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                                               - nucleic search, using sw model
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AC113332 Oryza sat AC113332 Oryza sat AC13665 Oryza sat AF49744 Aegilops AF49744 Aegilops AF49747 Aegilops BD012674 Method of BD012675 Method of BD012675 Method of BD012674 Method of AY248704 Aegilops Call Method of AY248704 Triticum ae AF256698 Aegilops AZ26698 Aegilops AZ368970 Triticum AJ308967 Triticum AF476960 Aegilops AY26914785 Thinopyru AZ681345 Thinopyru AZ68139 Penicilli AJ34785 Triticum AF476962 Aegilops AZ647697 Triticum AF476962 Aegilops AZ647697 Triticum AF216869 Triticum AZ114785 Aegilops AZ260549 Triticum AZ114785 Aegilops AZ260549 Triticum AZ1147159 Aegilops AZ260549 Triticum AZ1147159 Aegilops AZ260549 Triticum AZ1147159 Aegilops AZ260549 Triticum AZ1147159 AEGILOPS AZ260549 Triticum AZ260540 Triticum AZ2 PLN 22-OCT-2001 1 (bases 1 to 932) Woo,Y.M., Hu,D.W., Larkins,B.A. and Jung,R. Genomics analysis of genes expressed in maize endosperm identifies Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear AF371278 932 bp mRNA Zea mays alpha globulin mRNA, complete cds. ALIGNMENTS SUMMARIES AY268139 HVDNAHOR3 BD012675 BD012674 AY248704 ASU39229 TAGLU1DG AC139010 TAGLD12B AC113332 AC130605 TAE308967 **BLYHOR3** AF371278.1 GI:16305141 DB Length 102842 120562 Query *-----*Zea mays Zea mays Score 171.8 171.8 171.8 170.2 170.2 170.2 156.8 91.2 91.2 91.2 91.2 91.2 80 80 80 79.8 78.4 78.2 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE RESULT 1 AF371278 LOCUS 60-CO V3 Result

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esmpmpleogwsssssseyyggegssseggyygegsseegyygegopgmtrvrlitra
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19 kDa globulin; alpha-globulin; cereal storage protein; globulin.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhatroideae; Oryzaee; Oryzae; Oryzae; Oryzae; Oryzae; Lors, K.C., Huang, J.K., Pan, J.S.,
Hermodson, M.A., Tanaka, K., Muthukrishnan, S. and Reeck, G.R.
A novel cereal storage protein: molecular genetics of the 19 kDa
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Location/Qualifiers
Location/Qualifiers
1. 757
/ Organism="Moryza sativa (japonica cultivar-group)" / mol type="mmkN" | fatrain="Mipponbare (Japonica)" / fatrain="Mipponbare (Japonica)" / fatrain="Mipponbare (Japonica)" / fatrain="Mipponbare" / f
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                                                                                                      AGTACTAGCTACCATGGTTAAAGCGAGTCGGCGCGAGGTGCAAGACGCATGTGTACT
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/product="19 kDa globulin"
666. .672
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Jung,R.
Jung,R.
Direct Submission
Submitted (18-APR-2001) TTD, Pioneer Hi-Bred International, Inc. 7300NW 62nd Ave., Johnston, IA 50131, USA
Location/Qualifiers
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108. 728
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.

1 (bases 1 to 82s)
Krishnan, H.B. and Pueppke, S.G.
                                                                                                                                                                                                                                                                                                                                                                                                      GCGGCGCTGTGCTTCGCGCCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGAGGTCGAGCGG 197
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Oryza sativa DNA fragment with a miscellaneous signal and an open
reading frame.
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Location/Qualifiers
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/cultivar="lamont"
/db_xraf="taxon:39947"
/tisue_type="endosperm"
/dev_stage="20 days post-anthesis"
                                                                                                                                                                                                                                                      Score 171.8; DB 8;
Pred. No. 8e-18;
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/protein_id="AAA72362.1"
/db_xref="GI:169805"
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Tanaka, K. and Matsuda, T. Clouding dene: sequence clouhing of the rice seed alpha-globulin-encoding gene: sequence similarity of the 5'-flanking region to those of the genes encoding wheat high-molecular-weight glutenin and barley D hordein Gene 170 (2), 223-226 (1996)
/translation="MAAMVAISGAHVSESEMRFRDRQCQREVQDSPLDACRQVLDRQL
TGRERFQPMFRRPGALGLRMQCCQQLQDVSRECRCAAIRRMVRSYEESMPMPLEQGWS
SSSSEYYGGEGSSSEQGYYGEGSSEEGYYGEQQQQPGMTRVRLTRARQYAAQLPSMCR
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kDa globulin,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (22-MAY-1995) Masayuki Nakase, Nagoya University, Scho
of Agricultural Sciences, Applied Biological Sciences; Furo-cho,
Chikusa-ku, Nagoya, Aichi 464-01, Japan
(E-mail:145231a@nucc.cc.nagoya-u.ac.jp, Tel:052-789-4131,
Pax:052-789-4120)
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Pred. No. 8e-18;
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34084 GCGGCGGCTCATGGCGGCCATGTGGCGCGCGCGCGCGCAGTGAGCGAGTCGAG 34025
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AC130605.
AC130605.1 GI:22212956
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            La Jonger 1.C. and Chow, T.-Y.

Submittee (12-Man 2013) Institute of Botany, Academia Sinica, 12 Stubmittee (12-Man 2013) Institute of Botany, Academia Sinica, 12 Scution 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan Excellent (12-Man 2013) Institute of Botany, Academia Sinica, 12 Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan The mucleotide sequence of this BAC clone was generated by combining Monsanto and ASPGC-Taiwan sequence in the requencing data.

**NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be resplaced

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/note="japonica cultivar-group"
: 22452 c 22701 g 27030 t
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                                                                                                                                                                                                                                                              /product="26 kDa globulin"
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RQYAAQLPSMCRVEPQQCSIFAAGGY"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 99518)
Chow,T.-Y., Heling,Y.-I.C., Chen,C.-S., Chen,H.-H., Wu,H.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,T.-R., Chen,Y.-L., Chow,M.-H.J., Hong,Y.-C., Hailung,J.-N., Hau,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C., Leu,H.-L., Lin,S.-J., Wu,L.-F. and Shaw,J.-F. Oryza sativa BAC OJ1057_802 genomic sequence
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Chow, T.-Y. and Hsing, Y.-I.C.
Direct Submission
Submitted (01-MAR-2002) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 093 ATGAGGTTCAGGGACAGGCAGTGCCAGCGGGGGGGGGCAGGACAGCCCGCTGGACGCTGC
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                               /organism="Oryza sativa (japonica cultivar-group)"
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/db xref="taxon:39947"
/tisue_type="endosperm"
/dev alage="immature"
1009. .1569
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Location/Qualifiers
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VGRGGQRQGVGLCHKRPQRQQEGGFSGEGAQQKPQAGRVRLTKVRLPFACRIEPQECS
                                                                                                                                                                                           AF497474 linear PLN 15-JUL-2002 Aegilops tauschii leucine-rich-like protein gene, partial cds; seed globulin (Glo-2) gene, complete cds; HFW-glutenin (Glu-Dty) gene, Gulu-Dty-T2 allele, complete cds; and HFW-glutenin (HFW) gene, HFW-Dtx2 allele, complete cds.
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MSQLNKLILSINNNLEGSIPAFFGNLTFELISLDLSSNLLSGQIPBEVMSISSLSHVPLNL
MSQLDKTİTPHYGÇLYALIMDLSSNKLSSAİPVITGSSCIELQFLYLĞGNLLHĞQIP
KEFMALRĞLEELDLSSNNLSGPVPEFLESFQLLKNLNLSFNQLSGPVPDTGIFSNNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaes; Aggilops.

1 (bases 1 to 102842)
Anderson,O.D., Rausch,C., Moullet,O. and Lagudah,E.S.
Characterization of a wheat D-genome BAC containing two paralogous HMW-glutenin genes: distribution of genes and retrotransposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1 to 102842)
Anderson, O. D., Rausch, C., Moullet, O. and Lagudah, E.S.
Direct Submission
Submitted (28-MAR-2002) ARS, U.S. Department of Agriculture, 800
Buchanan Street, Albany, CA 94710, USA
Location/Qualifiers
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/note="CSIRO accession number AUS18913"
complement(<1. .>1959)
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    119462 CTGGAGCAAGGCTGGTCGTCGTCGTCGGAGTA 119428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSLTSNGMLCGGPVFFHFPACPYLAPDKL"
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<7856. .>9730
/gene="Glu-Dty"
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/gene="Glo-2"
<3320. .>4000
/gene="Glo-2"
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/gene="Glo-2"
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Aegilops tauschii
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                                                                                                                  RESULT 7
AF497474
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DEFINITION
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AUTHORS
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                        Oryza satīva (japonica cultivar-group)

Oryza satīva (japonica cultivar-group)

Bukaryota; Virīdiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 12413)

Chow, T.-Y., Hsing, Y.-I.C., Chen, H.-C., Chen, H.-H., Liu, S.-M.,

Chow, Y.-T., Chang, S.-J., Chen, H.-C., Chen, S.-Y., Hsing, Y.-I.,

Chao, Y.-L., Cheng, C.-H., Chung, C.-I., Han, S.-Y., Hsing, S.-M.,

Hsing, J.-N., Hsu, C.-H., Luang, J.-J., Kau, P.-I., Lee, M.-C.,

Leu, H.-L., Li, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Yu, C.-Y.,

Vu, S.-W., Wu, H.-P. and Shaw, J.-P.

Oryza sativa PAC POULDO4 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

Direct Submission

Submitted (13-AUG-2002) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 24826; contig of 24826 bp in length

* 24927 39423; contig of 14497 bp in length

* 39424 39523; gap of unknown length

* 39544 39533; gap of unknown length

* 39506 124132; contig of 34427 bp in length

* 89506 124132; contig of 34427 bp in length

* 89706 124132; contig of 34427 bp in length

* 10-cation/Qualifiers

//mol_type="genomic DNA"

//mol_type="genomic DNA"

//mol_type="genomic DNA"

//mol_type="genomic DNA"

//mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 CAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGAGCCCGCTCGACGCGTGC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 CGGTGGGGCACCGGGCTCCGGATGCGGTGCTGCCAGCAGCTCCAGGACGTGAGCCGCGAG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 TGCCGCTGCGCCGCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCATGCC---GCCG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 others
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27001 c 26916 g 35690 t
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/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 124132)
Chow, T.-Y. and Hsing, Y.-I.C.
Direct Submission
        HTG: HTGS PHASE2
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/ LTADELGALGSWITTRGTHOFTSTATALLHPSTSSSSYSTAHDLPALLSFKS
LITKOPICALGSWITTRGTHOFCSWITCHCSTATOLSFLKSFLGALGSGISSFLSFLGN
LITKOPICAGALSWITTRGTHOFCSWITCHCSWITCHCSWITCHCSFLOSFLSFLACHLOLGSGISFLSFLGN
LSRLADLDLGGNYLOGGIPPSSIGNCFALRTINLSVNSLGGAIPPAMGNLSKLLIVLSVS
KNDISGTIPTSFRGLATVAVESVARNHVHGQVPPWLCNITALEDLNWADNINGGHVPP
ALSKLINLASITVATINLOGIPPVINSSELLNFGSNGLGSGLPQDIGSMLDNLK
REGOIPASLISNISSLEHLSLHGARFRGIPSNIGGSGLPQDIGSMLDNLK
RTSRDWDFLFSLANNCSSLLLVNLQLNNLSGILDNSIGNLSQKLEGLRVGGNOIAGLI
ATTGRYRLALILEPANNRFTGTIPPSIGKLSKLELSGKIPSSIGNLSVAL
NLLALSTNNLEGSIPPTGGALTLSLLGSKILGSKILGSKILSNNL
LDGPISPHIGQLANLAIIDFSSNKLSGPIPNALGSCIALQFLHLQGNLLQGGIPKELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes
                                                                   3578 GAGTGCCGCTGCGCCCTCCGCGCATGGTGCGGGACTACGAGCAGTCCATGCCGCCG 3637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear PLN 07-MAY-2003
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/clone_lib="HV_MBa-Library, Clemson University of Genomics
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Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (Bases 1 to 120562)
2 (Bases 1 to Londeore, C.F., Kong, X., Chibbar, R.N. and
Lazo, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 120562)
Gu, Y.Q., Anderson, O.D., Londeore, C.F., Kong, X., Chibbar, R.N. and
Lazo, G.R.
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Submitted (03-APA-2003) ARS, U.S. Department of Agriculture, 800
Buchanan Street, Albany, CA 94710, USA
Location/Qualifiers
375 GAGTGCCGCTGCCCCCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCATGCCGCG
                                                                                                                                                                                                                                                      3638 cricocada a de concece con contra con contra con contra con contra con contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra con
                                                                                                                                                                     435 CTGGAGAAAGGCTGGTGGCCATGGGGGCGCCAGCAGCAGCCGCCGCCGCAGGG 487
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complement (725. 3761)

/transposon="LTR retrotransposon Usier_184G9-1"

complement (3770. 12377)

/transposon="LTR retrotransposon Bare-1_184G9-1"

complement (12363. 21304)

/transposon="LTR retrotransposon Usier_184G9-1"
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/product="putative receptor kinase"
complement (join(27857. 28230,28919. .31616))
/note="similar to rice XA21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare BAC 18469, complete sequece.
AY268139. GI:30421164
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/protein_id="AAP31049.1"
/db_xref="G1:30421165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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/note="Afal repeat"
<26271. .>26538
/note="Afal repeat"
27437. .27600
/transpogon="MITE Stowaway"
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|organism="Hordeum vulgare"
|mol_type="genomic DNA"
|db_xref="taxon:4513"
|chromosome="5"
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QPGQGQQSGQEQQGYDGPYHVSAEQQAASPMVAKAQQPATQLPTVCRMEGGDALSASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICCGGTGGGGCACCGGGATGCGGTGCTGCCAGCAGCTCCAGGACGTGAGCCGC 374
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16.7%; Score 158.2; DB 8; Length 102842;
Best Local Similarity 69.7%; Pred. No. 1.1e-15;
Matches 246; Conservative 0; Mismatches 98; Indels 9; C
                                                                                                                                                                                                                                                                                                       /protein_id="AAM77581.1"
/db_xref="GI:21779919"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAM77582.1"
/db_xref="G1:21779920"
                                                                                                                        7856. .9730
/gene="Glu-Dty"
/codon_start=1
/product="HMW-glutenin"
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/product="HMW-glutenin"
<7856. .>9730
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/product="HMW-glutenin"
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<61216..>63753
/gene="HMW"
/allele="HMW-Dtx2"
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/gene="HMW"
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38933 GCGGTGTTCCTGACGACCCTGGTGACCATCTCCGCCGCCCAAGGCGTGCTCGA---GCAG 38989
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THVTTRVMGTYGYCAPEYAMSGKLTKMSD I YCFGVVLLEL I TGRRA I DTTKPTREQI L
FLVEVLMLSLLHHPNLVTLLGYCTECDQKILVYEYMPLGSLQDHLLDLTPKSQPLSWH
                                                                                                 VHWAAPLFKDKKKFTKMADPLLDSKYPLKGLYQALAISSMCLQEBAISRPLISDVVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bare-1_184G9-58"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transposon="LTR retrotransposon solo-LTR Wham_184G9-2s"
complement(109157. .>109388)
/transposon="LTR retrotransposon Bare-1_184G9-6p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transposon="LTR retrotransposon solo-LTR Wham_184G9-2s"
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/transposon="LTR retrotransposon Wham_184G9-1p"
complement (+93655. .>95251)
/transposon="LTR retrotransposon Barbara_184G9-1p"
95284. .>98782
/transposon="LTR retrotransposon Usier_184G9-2p"
                                                                                                                                        LTFLADPNYDPPDDIEPLPISVPNYDKGISLREAEISLSGFEEKQVEDS"
                                                                                                                                                                                                             transposon="non-LTR retrotransposon Leva_184G9-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                egion complement(<119185. 120562)
/transposon="LTR retrotransposon Bare-1_184G9-6p"
32679 a 27422 c 28340 g 32121 t
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/transposon="LTR retrotransposon Bare-1_184G9-6p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'transposon="LTR retrotransposon Bare-1_184G9-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87266. .87285
/rpt_type=tandem
/rpt_uniterandem
Complement(87880. .89305)
/transposon=1LTR retrotransposon solo-LTR
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/transposon="LTR element Wobi_184G9-1p"
                                                                                                                                                                                                                                                                                                                                                                                   transposon="LTR element Wobi_184G9-1p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transposon="LTR element Egug_184G9-1"
109133. .109156
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16.5%; Score 156.8; DB 8;
Best Local Similarity 71.3%; Pred. No. 1.8e-15;
Matches 238; Conservative 0; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                  .>77855)
                                                                                                                                                                                                                                                                          /rpt_type=tandem
/rpt_unit=ta
complement(77378.
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/product="putative protein kinase"
join(64782. .64942,65077. .65414,65452. .65555,66035. .66224,
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DDWVAHLGDFGLAKIIRAEKSKQSLADQSCSVGIKGTIGYVAPEYGTGTEISVEGDVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRQILEHQLTGRAVGVRPFQAQWGARDRCCQQLESVSRGCRCSALRGMVRDYEQSMPP
LREGRRRSSGERQQEQGCSGESTAEQQQEVQGGQYGSETGESQQQQGGGYHGVTVGRG
GQQGGQMLCRERPQRQQQGGGFGFSGEGAQQKPKVGRVRLTKVRLPTACRIEPQECSVFS
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AVRWGAAARGTKREAGQETSTSETKKTKRKWGRGFCGWASHEVEBPLTSETKKTKRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (41245. .42179)
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complement (42180. .4238)
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complement (<42387. .>43152)
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                                                                                                                                                                                                                                          FAAPVSRLGLACCRGSARQRIKMGDVVKELGAIKQIIMASQNYASWSTKLY"
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38555. .38618
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GRGFCGMASHEAEEPLTSETKKKRKNVAASSEPDKKRWFKNKIWKKKKKAKNEQLATLV KEISLATKLNSAMHVNINLSMNICPTQTYEEHSGTYLRNLAVIAVKQLDKDGLQGNRE 24; Gaps

88; Indels

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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Hor3"
37. .2160
/gene="Hor3"
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Matches 178; Conservative
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ORGANISM
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                                                                                X84366.1 GI:671536
D hordein, Hor3 gene.
D hordein, Hor3 gene.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                            overlapping with that under the accession number X68072.
Location/Qualifiers
1. .1859
                                                                                                                                                                                                                                                                                      Submitted (01-FEB-1995) M.B. Sorensen, Carlsberg Laboratory, Department of Physiology, Gamle Carlsbergvej 1, DK-2500 Valby, DENMARK
                                                                                                                                                                                 Sorensen, M.B., Muller, M., Skerritt, J. and Simpson, D. Hordenin promoter methylation and transcriptional activity in wild-type and mutant barley endosperm woll. Gen. Genet. 250 (6), 750-760 (1996)
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                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare subsp. vulgare"
//organism="Genomic DNA"
//orfety="Bomi"
//db xref="taxon:112509"
//chromosome="5"
                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91.2; DB 8;
Pred. No. 5.1e-05;
                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="endosperm"
/clone lib="lambda Zap II"
/dev_stage="seed"
343. .349
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                                                1859 bp
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/clone="pHor3-1"
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/gene="Hor3"
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Sorensen, M.B.
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/gene="Hor3
                                                           H. vulgare Hor3 gene.
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                                                HVDNAHOR3
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HVDNAHOR3
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Submitted (06-JAN-1996) Naohiko Hirota, Plant Bioengineering
Research Laboratories, Sapporo breweries, Biotechnology department;
Kizaki 37-1, Nitas, Gunma 370-03, Japan
Kizaki 18applant@po.infosphere.or.jp, Tel:0276-56-1455,
Fax:0276-56-1605)
Location/Qualifiers
1. 2296
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/clone="DH4"
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LOESSLEACRRVVDQQLVGQLPWSTGLQMQCCQQLRDVSPECRPVALSQVVRQYEQOT
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D hordein; Hor3.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaee; Hordeum.
1 (bases 1 to 2296)
Hirota,N., Kuroda,H. and Ito,K.
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Barley Hor3 mRNA for D hordein, complete cds.
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191

227

446

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unclassified.

I (bases 1 to 2434)

S Hirota,N., Kihara,M. and Ito,K.

Hirota,N., Kihara,M. and Ito,K.

Method of production of barley reduced gel protein

Datent: WO 0111946-A 1 22-FEB-2001;

SAPPORO BREWERISE LTD,NAOHIKO HIROTA,MAKOTO KIHARA,KAZUTOSHI ITO

OS HORDHUM VULGARE (barley)

PD 22-FEB-2001

PP 16-AUG-2000 WO 2000JP005476

PR 16-AUG-1999 JP 99P 229696

PI NAOHIKO HIROTA,MAKOTO KIHARA,KAZUTOSHI ITO

PC A01HS/00,C12N15/10,C12N15/63

CC

FH KEY
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9.6%; Score 91.2; DB 6; Length 2380;
Best Local Similarity 61.4%; Pred. No. 5.1e-05;
Matches 178; Conservative 0; Mismatches 88; Indels 24
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    /organism="unidentified"

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/db_xref="taxon:32644"
757 c 626 g 37
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WO 0111946-A/1.
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TITLE Method of production of barley reduced gel protein
JOURNAL SAPPOND BREWRIES LTD, NACHIKO HIROTA, MAKOTO KIHARA, KAZUTOSHI ITO
MANENT OS HOrdenum vulgare (barley)
PD 22-PEB-2001
PP 16-AUG-2000 WO 2000JP005476
PR 16-AUG-1999 JP 99P 229696
PR 16-AUG-1999 JP 99P 229696
PI NAOHIKO HIROTA, MAKOTO V.
CC
CC
FH "
                    TTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHGQQTTVSPHQGQQTTVSPHQG
QQTTVSPHQGQQPGEQPCGFPGQQTTVSLHHGQQSNELYYGSPYHVSVEQPSASLKVA
KAQQLAAQLPAMCRLEGGGGLLASQ"
CHQQGGGFGGGLTTEQPQGGKQPFHCQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Indels
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Pred. No. 5.1e-05;
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1. .2380
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/db_xref="taxon:32644"
a 747 c 622 g 369
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2214. .2219
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/gene="Hor3"
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/gene="Hor3"
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2267. .2272
/gene="Hor3"
a 708 c
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Best Local Similarity 61.4%;
Matches 178; Conservative
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TITLE
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                                                                                                                                                                                  1063 TCCGAGATGTTAGCGCCCAAGTGCCGCCTCGCCATCAGCCAAGTCGAATATG 1122
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Aegilops tauschii high molecular weight glutenin subunit (Glu-1-2)
                                                                                                                                                                                                                                                                            298 GCGGCGCGTTGGGCCCGTTCCGGTGGGCCACCGGGCTCCGGATGCCGTGCTGCCAGCAGC 357
237
                                                                                                                                          238 AGAGCCCGCTCGACGCGTGCCGCCAGGTCCTCGACCGGCAGCTAACCGGCGGCGGCGGCG 297
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                                               178 GCCAAGGCGAGGTCGAGCGGCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGG
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Direct Submitted (24-OCT-1995) Amanda M. Mackie, Biological Sciences,
University of Sydney, Sydney, NSW 2006, Australia
Location/Qualifiers
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/note="8ubmitter'8 given name: Triticum tauschii"
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/gene="Glu-1-2"
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/gene="Glu-1-2"
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/gene="Glu-1-2"
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/gene="Glu-1-2"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
I (bases 1 to 2804)
In (bases 1 to 2804)
Aegilops tauschii Glu-1Dy12.1 gene coding for HWW glutenin subunit 1Dy12.1
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<858. .>2804

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<858. .>2804

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Zheng,J., Jiang,Y., Sun,M., Xiao,Y. and Yan,Y.
Direct Submission
Submitted (04-MAR-2003) Key Lab of Genetics and Biotechology,
Biology Department, Capital Normal University, Beijing 100037,
China
                                                                                                                                                                                  361 GGATCCTTCTACCCGGGGGGACCGCACCGCCGCTGCAGCAAGGAGGATG 410
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/mol_type="genomic DNA"
/isolate="TD151"
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note="sequence homologous to 5' end of a-gliadin gene"
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2513. 2518
/note="pot. polyA signal"
2516. 2521
/note="pot. polyA signal"
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                                                                                                                                    'note="1Dy-HMW-glutenin
                                 334. .340 // note="put. TATA-box"
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PGQGQQWYYPTSLQQPGQGQQGYYPTSLQQPGQGQQYYPTSLQHTGQRQQP
                                                                                                                                                                                              The central repetitive region between pos. 801 and 2270 is composed of two multiple repeated amino acid motifs: PGQGQQ and GYYPTSLQQ. Location/Qualifiers
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Wheat gene for HWM-glutenin subunit from chromosome 1D.
X03041
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Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.4%; Score 80; DB 8; Length 2809; Best Local Similarity 56.4%; Pred. No. 0.0031; Matches 186; Conservative 0; Mismatches 120; Indels
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202...218
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QVDOQLAGRLEPMETGAN COQULRDVSAKCRS VAVSQVARQYEQTVVPPRGGS FY

GETTPLAQLAGGI FWGTSGOTYQESYSTSPRQGSYY PGQASPQOPGGGOOGGY

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GORQQWYY PTSLQQPGGQQD IGKGKQCY FTSPGOLGGGOOGGYY PTSPQHT

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YPSLQQPGGGOOGHY PASLQQPGGOOGHY PASLQQPGGOOGHY PTSLQQLGGGO

IGQPGGCOOGHYP ASLQQPGGGOOGGOGGOOGGYY PTSLQQPGGOOGGYY PTSP

TSLQQPGGCOOGHYP ASLQQPGGGOOGGOOGGOOGGOOGGYY PTSP

OQPGGCOOGGYY PTSLQQPGGOOGGOOGGOOGGOOGGOOGGYY PTSP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AGICCACCBAGATGCCIAAGCGGCTGCTCTTTTGCGGCAGTAGTCATCGCCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 CTCTCACCACCGCTGAAGGTGAGGCCTCTAGGCAACTGCAGTGTGAGCGCGAGCTCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 AGAGCTCGCTTGAGGCATGCCGGCAGGTCGTGGACCAACAGTTGGCCGGTCG-----
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(aa 1-660)"
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OM nucleic - nucleic search, using sw model

Run on:

November 29, 2003, 13:28:03 ; Search time 2415 Seconds (without alignments) 9560.767 Million cell updates/sec

US-10-053-410-3 950 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

22781392 segs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

em\_esthum:\* em\_estin:\* em\_estov: \* em\_estpl: \* em\_estro: \* em\_estba:\*

em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•		Description	CC349094 OGUEN26TH	. AY105070 Zea mays	CC349105 OGUEN26TV	CA401604 EL01N0423
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	27 4 4 4 5 5 6 6 7 7 8 8 5 6 7 8 8 6 7 8 8 8 6 7 8 8 8 6 7 8 8 6 7 8 8 8 6 7 8 8 8 8		

## ALIGNMENTS

CC349094 915 bp DNA linear GSS 16-MAY-2003 OGURNZGTH ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0422E04, genomic survey sequence. CC349094 GC349094.1 GI:30818501 Zea mays		<pre>// Loases 1 to 355/ Whitelaw,C.3., Quackenbush,J., Van Aken,S., Utterback,T., Resnick ,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek ,R.W., Nunberg,A., Robbins,D. and Lakey,N.</pre>	Consortium for Maize Genomics Unpublished Contact: Cathy Whitelaw Tigg	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@cigr.org Seq primer: TR Class: sheared ends.
RESULT 1 CC349094/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	0 0 0 0 0 0 0 0 0	AUTHORS	TITLE JOURNAL COMMENT	

36

us-10-053-410-3.rst

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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
these are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                               HTC 16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assembles resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
CAATAATGATAATAACTATGAGGAATAAAATATGGGAATGTTGCCAGATAGTACTGGCGCC
                             95 CAATAATGATAATAACTATGAGGAATAAATATGGGAATGTTGCCAGATAGTAGTACTGGCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 900)
Hainey, C.F., Dolan, M. Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1.9e-80;
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                                                                                                              mRNA
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/db_xref="WaizeDB:635853"
/db_xref="taxon:4577"
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244 c 33
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Zea mays PCO101751 mRNA
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AY105070.1 GI:21208148
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Unpublished (2002)
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Zea mays
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     850
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                                                                                                                                                                                                                                                        RESULT 2
AY105070
LOCUS
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ACCESSION
VERSION
KEYWORDS
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                                                                                                /db_xref="taxon:4577"
/dlone="ZMMBMa0422E04"
/clone="Lb="ZM 0.7 1.5 KB"
/note="Vector: PBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
316 336 9 171 t
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                                                                                                                                                                                                                / Match 77.1%; Score 732; DB 29; Local Similarity 99.7%; Pred. No. 1.7e-64; nes 754; Conservative 0; Mismatches 0;
                                                                       /mol_type="genomic DNA"
/strain="B73"
 Seg primer: TF
Class: sheared ends.
Location/Qualifiers
1. .1038
/organism="Zea mays".
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Matches 754,
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                                                           GECGECGECGECGETTCGGTTCCGGTGGGCACCGGGCTCCGGATGCGGTGCTGC 307
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T., Citek, Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished
                                                                                                                                                                           428 CAGCCGCCGCCGCAGGAGGAGGAGGAGGACAGGGGGGCTACTACTCCCCTGCAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGGCGGCGACCAGTACTAGCTACCATGGTTAAAGCGAGTCGGCGCGAGGTGCAAGACG
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                                                                                                  351 CAGCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCATCCGGAGCATGGTCAGG
                                                                                                                                                                                                                                                                          CCAGGAGAGGGATACGCTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cathy Whitelaw
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CA402183 570 bp mRNA linear EST 07-NOV-2002 EL01N0432G05.g Endosperm_4 Zea mays CDNA, mRNA sequence. CA402183 GI:24767038
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1 (bases 1 to 570)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
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| organism="Zea mays"
| mol type="mkNA"
| cultivar="W2" |
| cultivar="W2" |
| bxref="txxxxx:4577" |
| tissue type="Endosperm of 7-23DAP" |
| clone lib="Endosperm 4" |
| note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                         570 CATCCGGAGCATGGTCAGGGCTACGAGGAGGAGCCCATGCCGCCTCTGGAGAAAGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTATCCACCGTGTCGTCCCGGCACCACCGCGGCGGCCGACCAAGATCGGCCGCGTGAG
                                                              799 CAGAATGACGTAGCTCTGACGTGGGCTCGCAATATTGTCGCGTGTTCGTTACAATAATGA
                                                                            143 CAGAATGACGTAGCTCTGACGTGGGCTCGCAATATTGTCGCGTGTTCGTTACAATAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Fiscataway, NJ 08854,
Tel: 732-445-5380
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
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Sequencing of the maize endosperm ESTs
Unpublished
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E.
Messing,J.
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        CA401604 674 bp mRNA linear EST
EL01N0423A08.g Endosperm_4 Zea mays cDNA, mRNA sequence.
CA401604
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                                                                                                                                                                                                                                             Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
Dr. Do Frelinghuysen Rd., Piscataway, NJ 08854,
                                                                                                                                                                                                           Sequencing of the maize endosperm ESTs
Unpublished
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                                                                                                                                                                                                                                                                                                                                           Email: jlai@wakaman.rutgers.edu
Seg primer: T7.
Locatlon/Qualifiers
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                                                                GI:24766450
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AI745997 539 bp mRNA linear EST 02-FEB-2000 605078E03.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
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Zea mays
Zea mays
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 539)
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                      592 CGGCGGCGGCGCCGGCCCGTTCCGGTGGGCGCCCCGGGTCCGGGTGGGCCCCA
                                                                                        532 GCAGCTCCAGGACCTGAGGCGCGGAGTGCCGCTGCGCCATCCGGAGCATGGTCAGGGG
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                                                                         GCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCATCCGGAGCATGGTCAGGGG
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Department of Biological Sciences
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Stanford University
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
92
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                                                                                                          CCAGGAGTGCAGCATCTTCCCGGCGGCGACCAGTACTAGCTACCATGGTTAAAGCGAGT
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contract: Walbot V
Department of Biological Sciences
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855 California Ave, Palo Alto, CA 94304, USA
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Fax: 650 725 8221
Email: walbotdestanford.edu
Plate: 609664 row: E column: 02.
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1. .560
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EL01N0432G05.b Endosperm_4 Zea mays CDNA, mRNA sequence.
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Pred. No. 2.3e-34;
0; Mismatches 25;
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                        Contact: Walbot V
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Plate: 665065 row: F column: 05.
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hes 519; Conservative 0
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/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DHS(alpha)"
/clone lib="605 - Endosperm cDNA library from Schmidt lab"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoR1;
Site_2: Xho1; Kernel endosperm cDNA library from Schmidt lab"
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(Dases 1 to 560)
Walbot, V.
Walbot, V.
Whalze ESTs from various cDNA libraries sequenced at Stanford University
Unpublished
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                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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                                                                                                               Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 385.2; DB 14; Length 473;
Pred. No. 8.3e-30;
0; Mismatches 8; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAAGATTTGTGAGGGTGATCC-GCGCTGAGAAGAGATGGCTAAGATCGCC
                                                                                                                                                                 Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuyeen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-5735
Email: jlai@waksman.rutgers.edu
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                                                                                                                                    Sequencing of the maize endosperm ESTs
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RESULT 10 BE917827

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DESIZUEZT S86 bp mRNA linear EST 29-SEP-2000 OV1_7 F02.gl_A002 Ovary 1 (OV1) Sorghum bicolor cDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 CTACGAGGAGACCATGCCGCCGCTGGAGAAGGCTGG-----TGGGGGGAGCAGCGCGCA 291
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                                                                                                                                                                                                                                                                                                                                      An EST database from Sorghum: ovaries of varying immature stages Unpublished Contact: Cordonnier-Fratt PM Laboratory for Genomics and Bioinformatics The University of Georgia, Department.of Plant Biology That Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 CATGCGCTACGGCCATCGGCCCGTTCCGGTGGGGCACCGGGCTCCGGATGCGGTGCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCATCCGGAGCATGGTCAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 GCCGCCGCCGCAGGGAGGAGGAGGACGACGGGGGCTACTACTACTCCCCTGCAGCCGGCC
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High quality sequence start: 3
High quality sequence stop: 584
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                                                                                                                                                        Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                     BE917827
BE917827.1 GI:10420322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                           (bases 1 to 586)
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Best Local Similarity
Matches 503; Conserv
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BM500544 1inear EST 14-FEB-2002
PAC000000000895 Pioneer AF-1 array Zea mays cDNA, mRNA sequence.
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                                                                                                                                                                                    307
 216
                                     190
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                                                                                                                                                                                                                        337 GGATGCGGTGCTGCCAGCAGCTCCAGGACGTGCCGCGAGTGCCGCTGCCGCCATCC 396
                                                                                                                                                                                                                                                                                              397 GGAGCATGGTCAGGGGCTACGAGGAGGCCATGCCGCCGCTGGAGAAAGGCTGGTGGCCAT 456
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(bases 1 to 367)
                  CCCTGGTGGCCGTGGCCAAGGCGAGGTCGAGCGGCAGAGGCTCAGGGACCTGC
                                                                        217 AGTGCTGGCAGGAGGTCCAGGAGACCCGCTCGACGCGTGCCGCCAGGTCCTCGACCGGC
                                                                                                                                                277 AGCTAACCGGCGGCGGCGGCGGCGCGTTTGGCCCGTTCCGGTGGGGCACCGGGCTCC
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Trait and Technology Development, Food and Feed Research
Pioneer Hi-bread international, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     368 GGAGCATGGTCAGGGGTACGAGGAGAGACCATGCCGCCGCTGGAAAGGCTGG-----T
                                                                                                                                                                                                                                                                                                                                                                                                          ------GGGCTACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                              517 ACCCCTGCAGCCGGCCAGGAGAGAGATACGGCTACGGTCAGGGTGGCCAGCGGCAGATGT
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109 c 130 g 51 t
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Pred. No. 2.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                        422 gegegenecheccechecc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patterns of gene expression
Unpublished
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Zea mays
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   157
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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                                                                                                                                 712
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                                                                                           433 CGCCGCAGGGATGCCGATGATGTGCCGGCTGTCGGAGCCCCAGGAGTGCAGCGTCTTCTC 492
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                      381
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1 (Dases 1 to 665)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: ovaries of varying immature stages
CGGCACCACCGCCGCGCGCCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCCGGGAGTA
                                                                                                                                 CGCCGCGGGGTTGCCGATGATGTGCCGGCTGTCGGAGCCCCCAGGAGTGCAGCATCTTCTC
                                                                                                                                                                                                       CGGCGGCGACCAGTACTAGCTACCATGGTTAAAGCGAGTCGGCGCGAGGTGCAAGACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AACAATTAGCTAGCAGATCAACAACTAGCGACAAAGATTTGTTAGTGA-----TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 362.6; DB 10
Pred. No. 1.2e-27;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: JEN REV
High quality sequence stop: 523
POLYA=No.
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OV1 7 F02.bl A002 Ovary 1
sequence.
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Sorghum bicolor
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BE917909.1 GI:10420483
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Matches 520
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AUTHORS
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CA402267 652 bp mRNA linear EST 07-NOV-2002
EL01N0434D06.g Endosperm_4 Zea mays cDNA, mRNA sequence.
CA402267
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                                                                                                                                                                            329 geracegreacegreaceaceaceaceacearerarecacerereresececesecaceacea
                                                                                                                                                                                                                                              269 GCGGGCCAAGGATCGGCCGCGTGAGGCTTNCGAAGGCCCCGGGAGTACGCCGCCGGGTTGC 210
                                                                                                                                                                                                                                                                                    CGATGATGTGCCGGCTGTCGGAGCCCCCAGGAGTGCAGCATCTTCTCCGGCGGCGACCAGT 726
                                                                                                                                                                                                                                                                                                                                                       ACTAGCTACCATGGTTAA-----AGCGAGTCGGCGCGAGGTGCAAGACGCAT 776
                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/mol type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/tissue type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 652)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 GCTACGGTCAGGGCCAGCGGCAGATGTATCCACCGTGTCGTCCCGGCACCACCGGCG
                                                                                            389 GAGGAGGAGGAGGACAGGGGGGGGTACTACTACCTTCAGCCGGCCAGGAGAGGGATGCG
                                                                        GCGGGCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCCGGGAGTACGCCGCGGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGIACTGIGCGCGTACAAATCCAGAATGACGTAGTTCTGACGTGGGCTCGCATTGTCC
                                      Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
clade, Panicoideae, Andropogoneae, Zea.
                                      10;
 Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 285; DB 14; Length 652;
Pred. No. 6e-20;
0; Mismatches 10; Indels 18
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuyeen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-5735
Email: jlai@waksman.rutgers.edu
   DB 9;
32.3%; Score 307.2; DB 9 93.3%; Pred. No. 5.3e-22; ive 0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing of the maize endosperm ESTs Unpublished
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Matches 359; Conservative
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                     Best Local Similarity 93.3
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/tissue_type="nucellar, embryo, and endosperm"
/dev stage="10-14 days post-pollination"
/lab_nost="DHS(alpha)"
/clone_lib="665 - Endosperm cDNA library from Schmidt lab"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
/ste_2: XhoI; Kernel endosperm cDNA library from Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1670620 389 bp mRNA linear EST 02-FEB-2000 605035H03.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
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1 (bases 1 to 389)
Walbot, V.
Maize STS from various cDNA libraries sequenced at Stanford University
University
                                                                                                                                                                                                                                                 240
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                                                                      61 ACAAGTGGCGACAGACAAAGATTTGTGAGGGTGATCCGCGCGTGAGAAGAGATGGCTAAGA
                                    AAAAAAACCCCCTCGTCGATCACCACCAAAGAACACGAGTAACTAGCAGCTAGCACATCAA
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
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/ Corganism="Sorghum bicolor"

/ Mol_type="mRNA"

/ Mol_type="mRNA"

/ Ab xrefe="taxon:4558"

/ Clone lib="Ovary 1 (OV1)"

/ Clone lib="Ovary 1 (OV1)"

/ Note="Organ: Mix of ovaries of varying immature stages

/ Note="Organ: Wor of ovaries"

/ Site_1: XhoI; Vector: pBluescript II from Lambda

Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made

from poly-A RNA in the cloning vector lambda ZAP II.

Clones to be acquenced were prepared by mass excision."
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae, Andropogoneae; Sorghum.
1 (bases 1 to 425)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                 CGTCTGCCAAGGCGAGGTCGAGGCGCCAGAGGCTCAGGACCTGCAGTGCTGGCAGGAGGT 232
                                    115
                                                                         394
                                                                                                            TAAGATCGCCGCGGCGGCGGCGGC---GGCGCTGTGCTTCGCGGCCCTGGTGGCCGTGGC 172
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                                                                                                                                                                                                                                                                                                                                  CGCCGCCGCCGCTTGGCCCCGTTCCCGTGGGCCTCCCGGATGCGGTGCTGCCA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
454
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                                                        61 ACAAGTGGCGACAG----ACAAAGATTTGTGAGGGTGATCC-GCGCTGAGAAGAGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%; Score 256.2; DB 10; Length 425;
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High quality sequence stop: 393
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BG048804.1 GI:12499929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                           694 AGGAGTGCAGCATCTTCTCCGGCGGCGACCAGTACTAGCTACCATGGTTAAAGCGAGTCG 753
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                                                                           334 TCCGGATGCGGTGCTGCCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCA
                                                                                                            1 TCCGGATGCGGTGCTGCCAGCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCCCA
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                        Gaps
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  Pred. No. 5.8e-17;
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Search completed: November 29, 2003, 15:52:57 Job time : 2422 secs

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-DE-GONZ_1/USFTO_spool/US10053410/runat_28112003_140756_27880/app_query.fasta_1.391
-DB-GenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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Ygapop 10.0 ,
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AY268139 Hordeum V
AJ366974 Aegilops
X03041 Wheat gene
AY245797 Triticum
AY263343 Thinopyru
AY263345 Thinopyru
AY263345 Thinopyru
AY26346 Thinopyru
AY29518 Thinopyru
AY29518 Thinopyru
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AY29518 Thinopyru
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AY264065 Thinopyru
AY298724 Thinopyru
U39229 Aegilops ta
BB012675 Method of
BD012675 Method of
X12929 Triticum ae
AY348704 Aegilops
AJ309967 Triticum
AF476962 Aegilops
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D50643 Oryza sativ
AC113332 Oryza sat
AC1313605 Oryza sat
K63990 O.sativa mR
L12252 Oryza sativ
AF497474 Aegilops
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AY174159 Aegilops
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AJ314767
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Triticum

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AF354289 Aegilops AF476960 Aegilops AY245578 Triticum

**AF354289** 

ALIGNMENTS

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Nakase,M., Hotta,H., Adachi,T., Aoki,N., Nakamura,R., Masumura,T., Tanaka,K. and Matsuda,T. Cloning of the rice seed alpha-globulin-encoding gene: sequence similarity of the 5'-flanking region to those of the genes encoding wheat high-molecular-weight glutenin and barley D hordein Gene 170 (2), 223-226 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear PLN 23-MAR-2002
DNA for 26 kDa globulin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakabe, M., Hotta, H., Adachi, T., Alvarez, A.M., Aoki, N., Nakamura, R., Masumura, T., Tanaka, K. and Matsuda, T. Gene cloning and characterization of rice seed 26 kDa globulin: sequence similarity of its 5'-flanking region to those of wheat high molecular weight glutenin and barley D hordein
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Submitted (22-MAY-1995) Masayuki Nakase, Nagoya University, School
of Agricultural Sciences, Applied Biological Sciences; Furo-cho,
Chikusa-ku, Nagoya, Aichi 464-01, Japan Tel:052-789-4131,
[E-mail:145231a@mucc.cc.nagoya-u.ac.jp, Tel:052-789-4131,
                                                           140
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26 kDa globulin.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza, viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhrhartoideae; Oryzese;
GCCTACGAGGAGGCCATGCCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGGCGGCAGCAG
                                                         GlnProProProGlnGlyGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrProCysSerArg
                                                                                                                                                                                                                                                           588 CCCGCCACCACCGCGCGCGCCCAAGGATCGCCCGCGTGAGGCTTACGAAGGCCCGGGAG
                                                                                              528 CCAGGAGAGAGATACGGCTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGT
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1009. .1569
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PGTTGGGCRGRIGRVRTKARREAAGLPWCRLSEPQECSIFSGGDQY"
259 c 334 g 140 t
                      PLN 22-OCT-2001
                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 932)

Woo, Y.M., Hu, D.W., Larkins, B.A. and Jung, R.
Genomics analysis of genes expressed in maize endosperm identifies novel seed proteins and clarifies patterns of zein gene expression plant Cell 13 (10), 2297-2317 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAla1leArgSerMetValArg 100
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                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-APR-2001) TTD, Pioneer Hi-Bred International, Inc.,
7300NW 62nd Ave., Johnston, IA 50131, USA
Location/Qualifiers
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Zea mays alpha globulin mRNA, complete cds.
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108. 728
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Chow, T.-Y. and Hsing, Y.-I.C.

Chow, T.-Y. and Hsing, Y.-I.C.

Chow, T.-Y. and Hsing, Y.-I.C.

Chow, T.-Y. and Hsing, Y.-I.C.

Chow, T.-Y. and Hsing, Y.-I.C.

Direct Submitted (01-MAR-2002) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan

B. Haing, Y.-I.C. and Chow, T.-Y.

Direct Submission

I. Submitted (29-MAR-2003) Institute of Botany, Academia Sinica, 128, Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan The mucleotide sequence of this BAC clone was generated by combining Monsanto and ASPCC-Taiwan sequencing data.

* NOTE: This is a "working draft" sequence: It currently

* consists of 5 contigs. dags between the contigs

* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34108 ATGCCTAGCAAGGTCGTCTTCTTCGCGGCGCGCTC---ATGGCGCCCATGGTGGCGCCATC 34052
Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Wu,H.-P.,
Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,T.-R., Chen,Y.-L.,
Chow,M.-H.J., Hong,Y.-C., Hsiung,J.-N., Hsu,C.-H., Huang,J.-J.,
Oryza sativa BAC 011657_B02 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 891 990: contig of 890 bp in length
* 991 19703: contig of 890 bp in length
* 19704 19803: gap of unknown length
* 15539 contig of 18713 bp in length
* 75539 contig of 55735 bp in length
* 75539 contig of 16852 bp in length
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    99538
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22452 c 22701 g 27030 t 4
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        LDACRQVLDRQLTGRERFQPMFRRPGALGLRMQCCQQLQDVSRECRCAAIRRMYRSYE
SEMPMILLEACAMSSSSBYYGGEGSSSEQYYGEGSSEEGYYGEQQQPGMTRVRLTRA
RQYAAAQLPSMCKVEPQCSIIFAAGQY"
448 c 448 g 406 t
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HTG; HTGS PHASE2.
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 nGlnGlnProProProGlnGlyGlyGlyGlyGlyGlnGlyGlyTyrTyrTyrProCysSe 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 -ProProCysArgProGlyThrThrGlyGlyGlyProArgIleGlyArgValArgLeuTh 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 rLysAlaArgGluTyrAlaAlaGlyLeuDroMetMetCysArgLeuSerGluProGlnG1 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 sGlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValAr 100
                                                                                                                                                                                                                                                                                                                                             MetAlaLysIleAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                              21 AlaValCysGlnGlyGluValGluArgGlnArgLeuArgAspLeuGlnCysTrpGlnGlu 40
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                              (japonica cultivar-group)"
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O.sativa mRNA for 19 kDa globulin.
K63990 S76663
K63990.1 G1:20158
19 kDa globulin; alpha-globulin; cereal
Oryza sativa (japonica cultivar-group)
                                                                                                                        35690
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        1. .124132
/organism="Oryza sativa
                                                                                                                                                                                                                                                                                              (1-124132)
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                                           /mol_type="genomic DNA
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="5"
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Location/Qualifiers
                                                                                                          /clone="P0010D04"
27001 c 26916 g
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GAGAGGTTCCAGCCGATGTTCCGCCGCCCGGGC-GCGCTCGGCCTGCGGATGCAGTGCTG 33873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear HTG 13-AUG-2002 chromosome 5 clone P0010D04, red pieces.
                             BG]nGlnLeuGlnAapValSerArgGluCy8ArgCy8AlaAlaIleArgSerMetValAr 100
                                                                                                                                                         139
                                                                                                                                                                                                                                                                              -ProProCysArgProGlyThrThrGlyGlyGlyProArglleGlyArgValArgLeuTh 176
                                                                                           gGlyTyrGluGluAlaMetPro---ProLeuGluLysGlyTrpTrpProTrpGlyArgGl 119
                                                                                                                                                                                                                    rArgProGlyGluGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyr----- 156
                                                CCAGCAGCAGGACGAGGACGCGCGGAGTGCCGCTGCGCCCATCCGCCGGATGGTGAG
                                                                                                             GAGCTACGAGGAGAGCATGCCCGTGGACCAAGGCTGGTCGTCGTCGTCGGA
                                                                                                                                                     nGlnGlnProProProGlnGlyGlyGlyGlyGlnGlyGlyTyrTyrTyrProCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chow.T.-Y. and Heing,Y.-I.C.
Chow.T.-Y. and Heing,Y.-I.C.
Chow.T.-Y. and Heing,Y.-I.C.
Chow.T.-Y. and Heing,Y.-I.C.
Submission
Submitted (13-ANG-2002) Institute of Botany, Academia Sinica, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
NOTE: This is a "working draft" sequence. It currently
consists of 4 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is balieved to be correct as given, however the sizes
tithe gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 24826 contig 0f 24826 bp in length

* 24927 39423 contig of 14497 bp in length

* 39524 89505; contig of 14497 bp in length

* 39524 89505; contig of 50082 bp in length

* 89506 89705; gap of unknown length

* 89706 124132; contig of 34427 bp in length.
                                                                                                                                                                                    GTACTAC-------GGCGGCGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC130605 124132 bp DNA Oryza sativa (japonica cultivar-group) chr *** SEQUENCING IN PROGRESS ***, 4 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                         33578 GTGCAGCATCTTCGCCGCCGGC---CAGTAC 33551
                                                                                                                                                                                                                                                                                                                                                                                                          uCysSerIlePheSerGlyGlyAspGlnTyr
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AC130605/c
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AUTHORS
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PLN 16-JUL-1993
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryza.

1. (bases 1 to 825)
Krishnan, H.B. and Pueppke, S.G.
Krishnan, H.B. and Pueppke, S.G.
Nucleotide sequence of an abundant rice seed globulin: homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 rLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCysArgLeuSerGluProGlnGl 196
                            sGlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValAr 100
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                                                           CCAGCAGCTGCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCATCCGCCGGATGGTGAG
                                                                                                                                                                                                                                                                                                                                                            406 GTCGTCGGAGCAGGGGTAC---TACGGCGAGGGGTCGTCGGAGGAGGGGTACTACGGCGA
                                                                                                                                                                           rArgProGlyGluGlyTyrGlyGlyGlnGlyGlyGlnArgGlnMetTyr-----
                                                                                                                                                                                                                                                                                                                                                                                                                               157 -ProProCysArgProGlyThrThrGlyGlyGlyProArgIleGlyArgValArgLeuTh
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/db_xref="GI:169805"
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Ldacrovldroltgrerpopmpprppgalglrmoccoolodvsrecrcaalrrmvrsyb
Esmpmpleogwssssseyyggegssseggyygegsseegyygegoomtrvrltra
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bkaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae; Oryzeae, Oryza
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                                                                                                                    Shorrosh, B.S., Wen, L., Zen, K.C., Huang, J.K., Pan, J.S., Hermodson, M.A., Tanaka, K., Muthukrishnan, S. and Reeck, G.R. A novel cereal storage protein: molecular genetics of the 19 kDa globulin of rice
                                                                                                                                                                                                                                                                                                                  Shorrosh, B.
Direct Submission
Submitted (17-MAY-1992) B. Shorrosh, The Samuel Roberts Noble Submitted (17-MAY-1992) B. Shorrosh, The Samuel Roberts Noble Foundation, Plant Biology Division, 2510-1990East, Ardmore, Oklahoma 73402, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
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Plant Mol. Biol. 18 (1), 151-154 (1992)
92119226
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/product="19 kDa globulin"
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              Unpublished
2 (bases 1 to 102842)
2 (bases 1 to 102842)
Direct Submission
Submitted (28-MAR-2002) ARS, U.S. Department of Agriculture, 800
Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                       /organism="Aegilops tauschii"
/mol_type="genomic DNA"
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/product="leucine-rich-like protein"
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/gene="Glu-Dty"
/product="HMW-glutenin"
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/gene="Glo-2"
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1 (bases 1 to 102842)

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Characterization of a wheat D-genome BAC containing two paralogous HWW-glutenin genes: distribution of genes and retrotransposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 yGlyGlyGlnGlyGlyTyrTyrTyrProCysSerArgProGlyGluGlyTyrGlyTyrGl 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 yGlyGlyProArgIleGlyArgValArgLeuThrLysAlaArgGluTyrAlaAlaGlyLe 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 CGGCAGGTGCTCGACCGGCAGCTCACCGGCCGGGAGAGGTTCCAGCCGATGTTCCGCCGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 CCGGGC-GCGCTCGGCCTGCGGATGCAGTGCTGCTGCTGCAGCTGCAGGACCTGAGCCGCGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLeuGluLysGlyTrpTrpProTrpGlyArgGlnGlnGlnBroProProGlnGlyGlyGl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 yGlnGlyGlyGlnArgGlnMetTyr-----ProProCyBArgProGlyThrThrGl 165
                                                                                                                                                                                                                                                                         29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                         |||||||
13 GCGGCGCTCATGGCGGCCATGTCCGATCTCCGGCGCGCACGTGAGCGAGTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ArgGlnValLeuAspArgGlnLeuThrGly-GlyGlyGlyGlyGlyGlyBlyProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||||
|CCTGGAGCAAGGCTGGTCGTCGTCGTGGAGTACTAC--------
                                                                                                                                                                                                                                                                      AlaalaLeuCysPheAlaAlaLeuValAlaValAlaValCysGlnGlyGluValGluArg
                                                                                                                                                                                                                                                                                                                                                                                   30 GlnArgLeuArgAspLeuGlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArgGl
                   825
106
19
49
29
              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                             Gaps:
                                                                                                                                                                                                                   (1-825)
                   1.04e-14
433.50
61.88%
52.48%
                                                                                                                                                                                                                   x RICMSF
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Aegilops tauschii
                                                                                                                                                                                                                US-10-053-410-4 (1-206)
                                                                       Percent Similarity:
Best Local Similarity:
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Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252
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                                                                                                                             Query Match:
DB:
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/clone="BAC 184G9"
/clone llb="HV_MBa-Library, Clemson University of Genomics
Institute"
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Litkdpligalsswitngsthgfcswigvecssahpghvkalrlogligsgtispplign
Lsrlkaldlsgnkloggoipssigncfalrtlnlsvnslsgaippamgnlskllvlsvs
                                                         3911 CGCGTGAGGTTGACGAAGGTGCGG-------CTGCCGACCGCGTGCCGGATC 3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN 07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vilgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
Pooideae, Triticeae, Hordeum.
1 (bases 1 to 120562)
Gu,Y.O., Anderson,O.D., Londeore,C.F., Kong,X., Chibbar,R.N. and
Lazo,G.R.
                            144 GlyTyrGlyTyrGlyGlyGlyGlyGlyGlnArgGlnMetTyrProProCyg-----ArgPro 161
                                                                                                                                                                                                                                                 172 ArgValArgLeuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCysArgLeu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-APR-2003) ARS, U.S. Department of Agriculture, 800
Buchanan Street, Albany, CA 94710, USA
Location/Qualifiers
1. 120562
/organism="Hordeum vulgare"
/mol_type="genomic DNA"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 120562)
Gu,Y.Q., Anderson,O.D., Londeore,C.F., Kong,X., Chibbar,R.N. and
Lazo,G.R.
                                                                                                                                    162 ------ProArglyGlyGlyGlyGlyGly
                                                                                                                                                                         complement (725. .3761)
/transposon="LTR retrotransposon Usier_184G9-1"
complement (3770. .12377)
/transposon="LTR retrotransposon Bare-1_184G9-1"
complement (12383. .21304)
/transposon="LTR retrotransposon Usier_184G9-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(<27857. .28230,28919. .>31616))
/product="putative receptor kinase"
complement(join(27857. .28230,28919. .31616))
/note="similar to rice XA21"
                                                                                                                                                                                                                                                                                                                                                                                     3956 ---GAGCCCCAGGAGTGTAGCGTCTTCACC---GCCGACCAGTAC 3994
                                                                                                                                                                                                                                                                                                                                                         192 SerGluProGlnGluCysSerIlePheSerGlyGlyAspGlnTyr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY268139
Hordeum vulgare BAC 184G9, complete sequece.
AY268139
AY268139.1 GI:30421164
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protein_id="AAP31049.1"
db_xref="G1:30421165"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <26067. .>26245.
/note="Afal repeat"
<2621. .>26538
/note="Afal repeat"
27437. .2760
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Hordeum vulgare
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AY268139
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PEGULO PARA CAGACA COPECA CAGACA SE ACACACA CAGACA CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3458 CAGATCCTCGAGCAGCAGCTGACTGGCCGCCGCGCGGGGGCGCCGTCGGCGTCG 3517
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                                                                                                                                                                                                                                                                                                                                                                                        translation="MAKRLVLFVAVVVALVALTVAEGEASEQLQCERELQELQEREL#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerArgGluCysArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGluAlaMet 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProProLeuGluLysGly---TrpTrpProTrpGlyArgGlnGlnGln------ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlyGlyGlyGlyGlyGlnGlyGlyTyrTyrTyrProCysSerArgProGlyGlu 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 ArgLeuArgAspLeuGlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArg
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                               protein_id="AAM77582.1"
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                                                                                                                                                                                                                                                                                                           product="HMW-glutenin"
                                                                                                                                                                                        /product="HMW-glutenin"
61216. .63753
                                                                                                                                                                                                                                                                                                                                                         xref="GI:21779920"
                 /rpt_family="rAGY-1"
<61216 .>63753
/gene="HWW"
/allele="HMW-Dtx2"
<61216 .>63753
/gene="HMW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
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414.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<64702. .64942,65077. .65414,65452. .65555,66035. .66224,66334. .66725,66880. .>67194)
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ALRGLEELDLSNNNLGSGPVPERLESPQLLKNIALSFYNILSGPVPDKGI FSNAGYISLY
SNGWLCGGPVPFHPPTCPY SEPDKLASHKLLQI LVFTANGA FILLGYCI AARCYVNKS
RGDAHQDQENT PEMFQRI SECKLAKMI FANDSFSEERULVGNGSFGSYYKGTGSGGAALITA
AVKVLDVQRQCAT FST I SECKLAKMI FHRKLVKVITVCDSLJHSGNOPKALVLEFI PN
GSLDKWLHPSTEDBFGT PNLMQRLNI ALDVAEALEYLHDHIDPPI VHCDVKPSNI LLD
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GQQQGQMLCRERPQRQQQGGGEGFSGEGAQQKPKVGRVRLIKKVRLPTACRIEPQECSVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALSKLINLRSLTVAINNLQGLIPPVLFNMSŠLECLNFGSNQLSGSLPQDIGSMLPNLK
KFSVFYNRFEGQIPASLSNISSLEHLSLHGNRFRGRIPSNIGQSGRLTVFEVGNNELQ
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                                                                                                                                                                                                                                                                                                                     DDMVAHLGDFGLAKI I RAEKSKQSLADQSCSVGI KGTI GYVAPEYGTGTEI SVEGDVY
SYGVLLLEMLTGRRPTDPFFSDTTNLPKYVEMACPGNLLETMDVNI RCNQEPQAVLEL
FAAPVSRLGLACCRGSARQKI KMGDVVKELGAI KQI IMASQNYASWSTKLY"
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QGQQPGEQPCGFPGQQTTVSLHHGQQSNELYYGSPYHVSVEQPSASLKVAKAQQLAAQ
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TTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHPGQQTTTVSPHPG
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SGS

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98
22
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62
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protein kinase'
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                       70339. .73731
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51.72%
42.24%
33.19%
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Best Local Similarity:
Query Match:
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Pred. No.:
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GHYPASQQELGQGQQGJIPASQQQPGQGQGHYPASLQQDFGQGQGHYPTSLQQLGQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 ACCACCGCTGAAGGTGAGGCCTCTAGGCAA-------CTACAGTGTGAGCGCGAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 CCACTGCAGCAACTCCAACAAGGAATATTTTGGGGAACATCTTCACAAACAGGTACAAGGG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetalaLysIleAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ValGinGluSerProLeuAspAlaCysArgGlnValLeuAspArgGinLeuThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 CAATATGAGCAAACTGTGGTGCCGCCCAAGGGCAGATCCTTCTACCCTGGTGAGACCACG
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80
25
51
65
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db_xref="GI:13992211"
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Matches:
Conservative:
Mismatches:
Indels:
                 gene="glu-1D-2"
function="seed storage protein"
                                                                                                                                                                                                                                                                                      SPMVAKAQOPATQLPTACRMEGGDALSASQ"
                                                                                                                                                                                                                                                                                                                                                                                                               224 t
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                                                                                                                                                                                                                                                                                                                                                                                 1Dy
                                                                                                                                                                                                                                                                                                                                   /evlue...
64. .1962
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/product="HMW subunit 1Dy
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673 c 516 g 22
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292.50
47.51%
36.20%
25.48%
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                                                                                                             39224 GAA-------GGGCGCCGCCGCTCGTCGGGGGAGCGTCAACAAGAGCGGGA 39268
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                                                                                                                                                                                                                                                                                                                                                                   ---CTACCGACCGCGTGC 39532
39050 CAGATCCTCGAGCATCAGCTGACC-----GGCCGCGCGCGTCGGCGTCCGGCCGTTTCAG 39103
                                                                                                                                                                                                                                                                                                                                                                                                                                            39428 CCGCAGCGGCAGCAGCAGGGAGAAGGGTTCTCCGGCGAGGGGGCGCAGCAGAACCGAAG 39487
                                                                                                                                                                                                                                                                                                                                                  160
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2 gene for glutenin HMW subunit
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AJ306874.1 GI:13992210
glu-1D-2 gene; glutenin HWW subunit 1Dy.
Aegilops cylindrica
Aegilops cylindrica
Rusaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Man, Y., Wang, D., Shewry, P.R. and Halford, N.G.
Isolation and characterization of five novel high molecular weight
subunit of glutenin genes from Triticum timopheevi and Aegilops
                                                                                                                                                                                                                    ------GinglyGlyTyrTyrTyrProCysSerArgProGly 142
                                                                                                                                                                                                                                                                                                                                                                                                               170 IleGlyArgValArgLeuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCys 189
                                                 ArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGluAlaMetProProLeuGlu
                                                                                                                                                                                                                                                                                                                                               143 GluGlyTyrGlyTyrGlyGlnGlyGlyGlpArgGlpAetTyrProProCysArg-----
                               TrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArgGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-APR-2001) Halford N.G., Crop Performance and Improvement, IARR-Long Ashton Research Station, Long Ashton Bristol, BS41 9AF, UNITED KINGDOM Location/Qualifiers
                                                                                                                                                                                                                                                                                                      39533 CGGATC---GAGCCCCAGGAGTGTAGCGTCTTCTCC 39565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgleuSerGluProGlnGluCysSerllePheSer 201
                                                                                                                                                        111 LysGlyTrpTrpProTrpGlyArg-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Aegilops cylindrica"
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|chromosome="1D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aegilops cylindrica partial glu-1D-2
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1. .1962
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Halford, N.G.
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Score: 289.50 Matches: 80 Percent Similarity: 47.06* Conservative: 24 Best Local Similarity: 36.20* Mismatches: 52 Query Match: 25.22* Indels: 65 DB: 8	AlaLeuCysP ::: GTAGTC ArgLeuArgA		624 CAGCAGCTCCGAGATGTTAGCGCCAAGTGCCCGCTCTCGCCGTCAGCCAAGAGAGTGCCCAAGTGCCCAAGAGTGCCCAAGTGCCCAAGAGTGCCCAAGTGCCCAAGAGTGCCCAAGAGTGCTCAGCCAAGAGTGCCAAGAGAGTGCCCAAGTGCCAAGAGTGCCAAGAGCCGCCCAAGAGCCGATCTTAGCCTTCTACCCTGGTGAGACCACGGTGCCCCCAAGGGCGGATCCTTCTACCCTGGTGAGACCACGGTGCCCCCAAGGGCGGATCCTTCTACCCTGGTGAGACCACGGTGAGACCACGGTGAGAGCCACGGTGAGAGCCACGGTGAGACCACGGTGAGAGCCACGGTGAGAGCCACGGTGAGAGCCACGGTGAGAGACCACGGTGAGAGAGCCACGGTGAGAGAGCCACGGTGAGAGACCACGGTGAGAGAGCCACGGTGAGAGAGA	Db 744 CCACTGCAGCAACTCCAACAAGGAATATTTTGGGGAACATCTTCACAAACAGTACAAGGG 803  Qy 118	Qy         134 TyrTyrTyrProCy8SerArgProGlyGluGlyTyrGlyGlyGlnGlyGly         151           bb         924 TGGTACTACCCAACTTCTTGCAGGACAAGGGCAACAGATAGGAAAAGGA980           Qy         152 GlnArgGlnMetTyrProProCy8ArgProGlyThrThrGlyGlyProArg11eGly         171           bb         981AAACAGGGTACTACCCAACTTCTTGCAGCAACAGGACAACAAATAGGA         1037           Qy         172 Arg         172           bb         1038 CAA         1040	RESULT 11 AY245797 LOCUS LOCUS DEFINITION Triticum turgidum subsp. durum HMW glutenin subunit 1By8 (Glu-1B) gene, Glu-1By8 allele, complete cds. AY245797 AY245797 AY245797 AY245797 VERSION VERSION AY245797.1 GI:29150725 SOURCE Triticum turgidum subsp. durum (durum wheat) ORGANISM Triticum turgidum subsp. durum (surum wheat) Friticum turgidum subsp. durum (surum wheat) Friticum turgidum subsp. durum subryophyta; Embryophyta; Embryophyta; Entricum turgidum subsp. durum Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooleaes; Triticeae; Triticaea; Triticaea; Pooleaes; Triticeae; Triticaea; AUTHORS Jiang, Y., Sun, M., Zheng, J., Xiao, Y. and Yan, Y. TITLE Durum wheat Glu-1By8 gene coding for HMW glutenin subunit 1By8 JOURNAL Unpublished
Db 439 CAACAGCCAGGACAACGCCAACCTGGCAAATGGCAAGAACCAGGACAAGGGCAACAA 498  Qy 134 TyrTyrTyrProCysSerArgProGlyGluGlyTyrGlyTyrGlyGlyGlyGly 151	Qy         152 GlnArgGlnWetTyrProProCygArgProGlyThrThrGlyGlyProArgIleGly 171           Db         :::	RESULT 10  TAGLUIDG LOCUS LOCUS LOCUS LOCUS  TAGLUIDG LOCUS  TAGLUIDG LOCUS  TAGLUIDG LOCUS  TAGLUIDG LOCUS  TAGLUIDG  TAGLUID	REFERENCE 1 (bases 1 to 3095) AUTHORS Thompson, R.D., Bartels, D. and Harberd, N.P. TITLE Nucleotide sequence of a gene from chromosome 1D of wheat encoding a HWW-glutenin subunit JOURNAL Nucleic Acids Res. 13 (19), 6833-6846 (1985) MEDLINE 86041882 PUBMED 3840588 COMMENT The central repetitive region between pos. 801 and 2270 is composed	of two multiple repeated amino acid motifs: PGGGQQ and GYYPTSLQQ. Location/Qualifiers Source 13095 / organism="Triticum aestivum" / mol_type="genomic DNA" / db_xref="taxon:4565" misc_feature 202218 / note="sequence homologous to 5' end of a-gliadin gene" / note="mit Tata_box"	CDS / ACC. 12408 / note="1Dy-HMW-glutenin (aa 1-660)" / codon start=1 / codon start=1 / protefin id="CA26847.1" / db_xref="Gi:11779" / db_xref="Gi:11779" / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / translate ion="MAKRIVILFARVIALTTARGEASRQLQCERELQESSLEACR / QVVDQQLAGRIPWGTSSQTYQGYYYPSVTSRQQSQQQDPGGQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	GHYPASQQEPGGGGGGTPASCAGATTATATATATATATATATATATATATATATATATAT

150

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Triticum aestivum glu-1R gene for high molecular weight glutenin subunit y, clone pAHTas1R11.
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/note="lR addition line obtained from T.aestivum cv.
Chinese Spring and S. cereale cv. Imperial as donor of 1R
                                                                                                                                                                                                                                                                                                                                                                          607 GGATACTACCCAACTTCTCTGCAGCAGCCAGGACAAGGGCAACAGATAGGACAAGGACAA 666
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Characterisation and analysis of new HWW-glutenin alleles encoded by the Glu-R1 locus of Secale cereale
Theor. Appl. Genet. 107, 74-83 (2003)
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Submitted (21-MAY-2001) De Bustos A., Cell Biology and Genetics,
University of Alcala, Campus Universitario, 28871 Alcala de
Henares, Madrid, SPAIN
                                                                                                                                                                                                                                                                                                                                               135 TyrTyrProCysSer----ArgProGlyGluGlyTyrGlyTyrGlyGlnGly-----
                                                                              367 ACAGTACAAGGGTATTACCCAAGCGTAAGTTCTCCTCAGCAGGGGCCATATTATCCAGGC
                                                                                                                                                                                 427 CAAGCTTCTCCACAACAGCCAGGACAAGGGCAACAGCCAGGCAAATGGCAAGAACTGGGA
                                                                                                                                                                                                                                                                                           153 ArgGlnMetTyrPro-----ProCysArgProGly------ThrThrGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 CAAGGGTACTACCCAACTTCTCCGCAACACCCAGGACAAAGGCAACAACAGGACAAGGG
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727 CAGCAAATAGGACAAGGGCAACTAGGACAAGGGCGGCAAATAGGACAAGGG 780
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Characterization of two gene subunits on the 1R chromosome as orthologe deach of the Glu-1 genes of hexaploid wheat Theor. Appl. Genet. 103, 733-742 (2001)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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AJ314785.1 GI:14329762
2]u-1R Gene; high molecular weight glutenin subunit
Triticum aestivum (bread wheat)
                                GlnGlnGlnPro
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/mol_type="genomic DNA"
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140. .2302
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                                                                                                                                                                                                                                       129 GlyGlyGlnGlyGlyTyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome
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                Jiang, Y., Sun, M., Zheng, J., Xiao, Y. and Yan, Y.
Direct Submission
Submitted (O3-MAR-2003) Key Lab of Genetics and Biotechnology,
Biology Deparment, Capital Normal University, Beijing 100037, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AÃO64642.1"
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SPQPQCQGCQXQCYYPTSPQQPGQQDQGQQQQGQCHCPTSPQQTGQAQQPGQQQ
IGQVQQPGQQQQCYPTSLLQSGCGQQSGQGQQSGGGHQLGQGQQQSGDEQQGYDNPYH
VNTEQQTASPKVAKVQQQPATQLPIMCRNEGGDALSASQ"
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Thinopyrum elongatum clone pUCG2b high molecular weight glutenin
y-subunit gene, complete cds.
  ------GlyGln 152
                                                                                                                                                                                                        746 GGATACTACCCAACTTCTCTGCAGCAGCCAGGACAAGGGCAACAGATAGGACAAGGÀCÀÀ 805
                                                                                                                                                                                                                                                          153 ArgGlnMetTyrPro-----ProCysArgProGly-----ThrThrGlyGlyGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thinopyrum elongatum kentura streptophyta; Embryophyta; Tracheophyta; Sparmatophyta; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Booideae; Triticeae; Thinopyrum. I (bases I to 1980)
Xia, G.M., Feng, D.S. and Chen, F.G.
Agropyron elongatum high molecular weight glutenin y-subunit gene
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2 (bases 1 to 1980)
2 (bases 1 to 1980)
2 Mard.W. Feng.D.S. and Chen,F.G.
Direct Submission
Submitted (25-MAR-2003) Plant Cell Engineering Laboratory, School of Life Science, Shandong University, Shan Da Nan Road 27, Jinan, Shandong 250100, China
Location, Qualifiers
                                                  135 TyrTyrProCysSer----ArgProGlyGluGlyTyrGlyTyrGlyGlnGly----
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806 caagggtactcaacttctccgcaacacccaggacaaggcaacaacaggacaagg
                                                                                                686 TACTACCCATCTTCTCTGCAGCAACCAGGACAAGGGCAACAAGATAGGACAAGAGGCAACAA
                                                                                                                                                                                                                                                                                                                                                        168 ProhrgileGlyArg---ValArgLeuThrLysAlaArgGluTyrAlaAlaGly 184
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IGOVQQPGGGGGYYPISLQQSGQGGQSGQGGGGHCPTSPQGFGQAQQ
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/evidence=experimental
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Theor. Appl. Genet. 75, 117-126 (1987)
2 (bases 1 to 2996)
Halford,N.G.
Direct Submission
Submitted (22-JUL-1991) N.G. Halford, Long Ashton Research Station,
University of Bristol, Dept. of Agricultural Sciences, Long Ashton,
Bristol BS18 9AF, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           793 CTCGTGGCTCTCACTGCTGCTGAAGGTGAGGCCTCTAGGCAA------CTACAG
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85
24
47
102
                                                                                                                                                                                                                                                               /tissue_type="endosperm"
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/gene="Glu-1By9"
814. .2865
/gene="Glu-1By9"
/product="HWW glutenin subunit 1By9"
2972. .2977
                                                                                                                                                                                                                                                                                                                                                                                                                                  product="HMW glutenin subunit 1By9"
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Mismatches:
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    2996
    /organism="Triticum aes
/mol_type="genomic DNA"
/cultivar="Cheyenne"

                                                                                                                                                                                                                          /db xref="taxon:4565"
/clone="lambda/HMW47"
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660. .666
                                                                                                                                                                                                                                                                                                                                       751. .2868
/gene="Glu-1By9"
751. .2868
/gene="Glu-1By9"
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AUTHORS
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Glu-1By9 gene; glutenin.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Triticum.
1 (bases 1 to 2996)
Halford,N.G., Forde,J., Anderson,O.D., Greene,F.C. and Shewry,P.R.
The nucleotide and deduced amino acide sequences of an HWW glutenin aubunit gene from chromosome 1B of bread wheat (triticum aestivum
L.) and comparison with those of genes from chromosomes 1A and 1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLN 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                       259 CAATATGAGCAAAACTGTGGTGCCGCCCAAGGGCGGATCCTTCTACCCTGGTGAGACCACG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 GlnGlyGlyTyrTyrTyrProCysSer-----ArgProGlyGluGlyTyrGly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnGlyGlyGlnArgGlnMetTyrProProCysArgProGlyThrThrGly----- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||
613 CAAGGG-----CAACAAGGGTACTACCCAACTTCTCCACAGCAAGGAAAAGGCAA 666
                                                                                                                                                                                        55 ACCACCGCTGAAGGTGAGGCCTCTAGGCAA------CTACAGTGTGAGGCGCGAG 102
                                                                                                                                                                                                                                            319 CCACTGCAGCAACTCCAACAAGAATATTTTGGGGAACATCTTCACAAACAGTACAAGGG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 TATTACCCAAGCGTAACTTCTCCTCGGCAGGGGTCATATTATCCAGGCCAAGCTTCTCCA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GlyArgGlnGlnBro-------ProproglnGly----- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 CAACAGCCAGGACGAGGCCAACAGCCTGGCAAATGGCAAGAACCAGGACAAGGGCAACAA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GlyGlyGlyGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 TGGTACTACCCAACTTCTCTGCAGCAGCCAGGACAATGGCAACAGATAGGAAAAGGGAAA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612
                                                                                                                                                  21 AlaValCysGlnGlyGluValGluArgGlnArgLeuArgAspLeuGlnCysTrpGlnGlu 40
                                                                                                                                                                                                                         41 ValGlnGluSerProLeuAspAlaCysArgGlnValLeuAspArgGlnLeuThrGlyGly 60
                                                                                                                                                                                                                                                                                               61 GlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCys 80
                                                                            MetAlaLysIleAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal 20
                                                                                                   1 ATGGCTAAGCGGCTGGTCCTCTTTGCGGCAGTAGTC-----ATCGCCCTCGTGGCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 CAAGGG-----TACTACCCAGCTTCTCTGCAGCAACCAGGACAAGGCCAACAAATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyTyrGluGlu---AlaMetProProLeuGluLysGlyTrpTrpPro
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Wheat Glu-1By9 gene for HMW glutenin subunit 1By9.
X61026
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         Gaps:
                                         US-10-053-410-4 (1-206) x AY263343 (1-1980)
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TITLE
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X61026
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/translation="MAKRLVLFATVVLALMALTAAEGEASRQLQCERELQESSLEACR
QVDQQLAGQLPWSTGLQMRCCQQLRDVSAKCRLTAVSQVVARQYEQQTAVPPKGGPFY
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QPGGCQQSGKGQQFGQGGGARASSPRHSCWQCAGWSGATHCRPGGGQGGYYPTSLQ
QPGGCQQSGKGQQFGQGTQDPGQGTQDPGQGGCGCGCGYSDSPYHVSARQQAAGLKVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGluGlyTyrGlyTyrGlyGlnGlyGlyGln---ArgGlnMetTyrProProCyBArg 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 TACCCCGGGGGAGCCGCCGCCACCGCAGCAACTACTTTGGGGAAGATCT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 CAGATGCGGTGCTGCCAGCAGCTCCGAGATGTTAGCGCCAAGTGCCGCCTCATCGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ArgSerMetValArgGlyTyrGluGlu-----AlaMetProProLeuGluLysGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 AGCCAAGTCGCAAGAACAATACGAGCAACAAAAACCGCGGTGCCGCCCAAGGGCGGACCCTTC
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                                                                                                                                                                                                                                                                                                                                                           36 GlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArgGlnValLeuAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GinLeuThrGlyGlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 CAGTTG------CCTGGCCAGCTGCCATGGAGCACGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 TCAGAAACAGTACAAGGGTATTACCCAAGCGTAACTTCTCCTCAGCGGGGGGTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 CCAGGCAAAGCTTCTCCACAACAACCAGGACAAGGGCAACAGCCAGGACAATGGCAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 AAAGCGCGCAGCAGCCCTCGACACAGCTGTTGGCAATGTGCCGGATGGAGTGGGGCGACG
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                                                                                                                                                                                                                                                                                                                                       AlaLeuValAlaValAyalCysGlnGlyGluValGluArgGlnArgLeuArgAspLeu
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Thinopyrum elongatum clone pUCG7a high molecular weight glutenin
y-gubunit gene, complete cds.
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Thinopyrum elongatum
Thinopyrum elongatum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vindiplantae, Streptophyta; Embryophyta; Pooleae;
Pooldeae; Triticeae; Thinopyrum.
I (Dases I to 906)
Xia,G.M., Feng, D.S. and Chen, F.G.
Agropyron elongatum high molecular weight glutenin y-subunit gene
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Jinan,
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caagggractaccaactrcrccaacaacaccaacaacaacaacaaggacaaggg
                                                        SerMetValArgGlyTyrGluGlu---AlaMetProProLeuGluLysGlyTrpTrpPro
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                                                                                                                              -----TrpGlyArg-----
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                                                                                                                                                                                                 ----GlnGlnGlnPro-
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Xia,G.M., Feng, D.S. and Chen, F.G.
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<sup>202</sup> GlyGlyABp 204 ||||||||||| 874 GGGGCCAC 882

Search completed: November 29, 2003, 18:16:13 Job time : 3585 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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November 29, 2003, 17:10:31; Search time 2046 Seconds (without alignments) 2447.078 Million cell updates/sec OM protein - nucleic search, using frame\_plus\_p2n model Run on:

1148 1 MAKIAAAAAAALCFAALVAV......MKRLSEPQECSIFSGGDQY 206 0.0 0.5 0.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-10-053-410-4 **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

45562784 22781392 seqs, 12152238056 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=Cqqq1 21VGPTO spool/VS10053410/runat 28112003 140757 27896/app query.fasta\_1.391
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EST:\* Database

hum: em\_estfun:\* em\_estom:\* em\_gss hum em\_esthum:\* em\_estin:\* em\_estro:\* em\_htc:\* gb\_estl:\* em\_estov:\* em\_estpl:\* em\_estba:\* est4:\* est3:\* gb est5:\* gb est2:

em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* #: m¤ш pro:\* fun: em\_gss\_pln: em\_gss\_vrt:

## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	AY105070 Zea mays	CC349094 OGUEN26TH	'n	4	605064	<b>-</b> 0	BEST/909 OVI / FOZ	, ,	A1712201 605065F05		4 OV1 2	0V1_23	AU164031 AU164031	605035H	AU163963	BQI/2/99 IUU8QU4 r	A1109459	1 WHE358	AU164041	AU16386	5 AU16397	0 AU16386	839 AU16383	642 AU09464	8 AU16396	043 AU16404	571 AU09457	635 AU09463	AU165812 AU165812	במשקוות שנים	6 AII16401	0 AU09457	3 AU16385	AU09456	0 AU09191	7 EL01NO	7 AU094637	4 PAC000	7 AU16579	000 AU16400	53999 AU1639	B AU16387	
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## ALIGNMENTS

HTC 16-OCT-2002 Zea mays Zea mays Zea mays Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. linear mRNA Zea mays PCO101751 mRNA sequence. AY105070.1 GI:21208148 HTC. DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AY105070 LOCUS

REFERENCE

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935 bp DNA linear GSS 16-MAY-2003
_0.7_1.5_KB Zea mays genomic clone ZMMBMa0422E04,
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                                                           161 ProGlyThrThrGlyGlyGlyProArgIleGlyArgValArgLeuThrLyBAlaArgGlu
488 CCAGGAGAGGATACGGCTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGT
                                                                                                    548 CCCGGCACCACCGGCGGCGGCCCAAGGATCGGCCGCGCGTGAGGCTTACGAAGGCCCCGGGAG
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methylation filtered genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., R.W., Nunberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA PEL: 301-838-5643 Fax: 301-838-0208 Email: whitelaw@tigr.org
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                                                                                                                                    Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAlalleArgSerMetValArg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part. of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 331 g 134 t
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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library:
  Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Unpublished (2002)

2 (bases 1 to 900)
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1 (bases 1 to 674)

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1 (bases 1 to 674)

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Matches:
Conservative:
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Zea mays
Eukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarotyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarotyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases I to 1038)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick
A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek
Consortium for Maize Genomics
Unpublished
                                                    80
                                                   GlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCySCyS
                 114 GTCCAGGAGACCCCCTCGACGCGTGCCGCCAGGTCCTCGACCGGCAGCTAACCGGCGC
                                                                     ValGlnGluSerProLeuAspAlaCysArgGlnValLeuAspArgGlnLeuThrGlyGly
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/clone_lib==zM_07_1.5_KB"
/note="vbc="zM_07"; Site_1; HincII; 0.7-1.5 kb
methylation filtered genomic_DNA libxary"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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GSS.
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TIGR
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 602)
Walbot, V.

Malbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 ArgSerMetValArgGlyTyrGluGluAlaMetProProLeuGluLysGlyTrpTrpPro
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A1711821
A1711821.1 GI:5005759
EST.
Zea mays
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Matches:
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Mismatches:
Indels:
         Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelingluysen Rd., Piscataway, NJ 08
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq priner: T7.
Location/Qualifiers
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490 115 430 133 370 153 310 173 250 193

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/organism="Sorghum bicolor"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:458"
/clone_lib="Toxor; 1 (Ov1)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site 1: Xhoi; Site 2: EcoRi; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
clones to be sequenced were prepared by mass excision."
184 c 217 g 82 t
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 30.20
Email: mmpratt@uga.edu
Email: mapratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                       Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 605)
                      TyrGluGluAlaMetProProLeuGluLyBGlyTrpTrpProTrpGlyArgGlnGlnGln 121
                                              ProProGlnGlyGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrTyrProCysSerArgPro 141
                                                                                                                                 ------GGCTACGACTACCCCTGCAGCA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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High quality sequence stop: 523
POLYA=No.
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BE917909.1 GI:10420483
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//organism="Sorghum bicolor"
//mol_type="manny"
//db_xref="taxon:4558"
//db_xref="taxon:4558"
//dolone_lib="cvary 1 (0V1)"
//note="Organ: Mix of ovaries of varying immature stages from 8 week-old plants; Vector: pBluescript II from Lambda 2ap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda 2AP II.
Clones to be sequenced were prepared by mass excision."
a 179 c 212 g 80 t
                                                                                BE917827 586 bp mRNA linear EST 29-SEP-2000 OV1_7_F02.g1_A002 Ovary 1 (OV1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 586)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GlyGlyGlyCalGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGln 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tal: 706 542 1860
Fax: 706 583 0210
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112
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16
16
189 CCCCAGGAGTGCAGCGTCTTCTCCGGCGGCGACCAGTAC 151
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High quality sequence start: 3
High quality sequence stop: 584
POLYA=No.
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Contact: Cordonnier-Pratt MM
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/mol_type="mRNA"

/cultivar="Chip43"

/db_xref="taxon.4577"

/tissue_type="nucellar, embryo, and endosperm"

/tissue_type="logo post-pollination"

/dev_stage="logo post-pollination"

/lab_host="DHS(alpha)"

/clone_lib="605 - Endosperm cDNA library from Schmidt lab"

/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoR1;

Site_2: XhoI; Kernel endosperm cDNA library from Schmidt

lab"
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EL01N0432G05.b Endosperm_4 Zea mays cDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                      172 ArgValArgLeuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCysArgLeu
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1131
12 1
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Unpublished
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
                                                                                                                                                                           105
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                             organism="Zea mays"
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Messing,J.
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CD443922.1 (
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Best Local Similarity:
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Zea mays
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AI745997.
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855 California Ave, Palo Alto, CA 94
721: 650 723 2227
Fax: 650 725 8221
Fax: 607 725 8221
Faxi: walbot@stanford.edu
Plate: 605078 row: E column: 03.
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| organism="Zea mays" |
| organism="Zea mays" |
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| cultivaz="Ohio43" |
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| /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI; Site_2: KhoI; Kernel endosperm cDNA library from Schmidt lab" |
| lab" |
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EST. Zea mays
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University
L Unpublished
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Flate: 60565 row: F column: 05.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                Waksman Înstitute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seg primer: T3.
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sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/organism="Zea mays"

/mol type="mRNA"

/culfivaz="W2"

/b xref="taxon:4577"

/tisue type="Endosperm of 7-23DAP"

/clone lib="Endosperm 4"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

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                                                    1 (bases 1 to 570)
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. Messing, J.
                                                                                                                                                                     Contect: Lai, Jinsheng
Dr. Joachim Messing's lab
Wakaman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T7.
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                                                                                                                                  Sequencing of the maize endosperm ESTs
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Sorghum bicolor (sorghum)
Sorghum bicolor
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/ Coganism=Sorghum bicolor"

/ Acganism=Sorghum bicolor"

/ Acganism=Sorghum bicolor"

/ Ab xref="taxon:4558"

/ Clone lib="Ovary 1 (OV1)"

/ Clone lib="Ovary 1 (OV1)"

/ Note="Organ: Mix of ovaries of varying immature stages

/ Note="Organ: Mix of ovaries of varying immature stages

from 8-week-old plants; Vector: pBluescript II from Lambda

Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made

from poly-A RNA in the cloning vector lambda ZAP II.

from poly-A RNA in the cloning vector lambda ZAP II.

127 c be sequenced were prepared by mass excision."
                                                                                                                                                          The Tata database from Sorghum: ovaries of varying immature stages Unpublished Contact: Cordonnier-Pratt MM Contact: Cordonnier-Pratt MM Contact: Cordonnier-Pratt MM Contact: Cordonnier-Pratt MM Contact: Cordonnier-Pratt MM Cordon Selection of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860
Fax: 706 583 0210
Fax: 706 583 0210
Fax: 706 bean trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 ArgSerMetValArgGlyTyrGluGluAlaMetProProLeuGluLysGlyTrpTrpPro 115
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High quality sequence stop: 393
POLYA=No.
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Best Local Similarity:
Query Match:
DB:
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AU164031 AUSON BANNA Linear EST 03-APR-2002 SULLYVAR-GROUP) CDNA clone E11772, mRNA sequence.
                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukartora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
1 (bases I to 683)
3 Sasaki, T. and Yamamoto, K.
Rice CDNA from panicle at ripening stage (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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/de_stage="ripening stage"
/clone lib="Rice panicle at ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ripening
124 cadcricacidedecedadaderrecadecearorrececedecededecedeceredecer
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-298-38-7468
Email: teasakl@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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                                                     1 others
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53.06$
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Tel: 81-298-38-7441
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/organism="Sorghum bicolor"
/mol type="maknA"
/db xref="taxon:4558"
/clone lib="towary 1 (0v1)"
/clone lib="rowary 1 (0v1)"
/note="forgan: Mix of ovaries of varying immature stages
from 8 week-old plants; vector: pBluescript II from Lambda
Zap II; site l: Khol; Site 2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
                                    97 496 bp mRNA linear EST 25-JAN-2001
_C05.91_A002 Ovary 1 (OV1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                           and Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ArgValArgLeuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCysArgLeu 191
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                                                                                                                                                                                                                                                                                          An EST database from Sorghum: ovaries of varying immature stages
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Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Esservent of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                   (bases 1 to 496)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M.
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                                                                                                                                           Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                          BG049097.1 GI:12500510
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
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Fax: 706 583 0210
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A1670620
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1 (bases 1 to 389)
Walbot, V.
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Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbocestanford.edu
Plate: 605035 row: H column: 03.
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APPLICANT: HIROTA, NACHIKO
APPLICANT: HIROTA, MACHIKO
APPLICANT: HIROTA, HISAC
APPLICANT: HISACOTO
APPLICANT: ITC, KAZUTOSHI
TITLE OF INVENTION: EXPRESSION REGULATORY DNA,
TITLE OF INVENTION: EXPRESSION CASSETTE, EXPRESSION VECTOR AND TRANSGENIC
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ALLINGTON
STARET: U.S.A.
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FILING DATE: 23-JUL-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP HEI 8-193433
FILING DATE: 23-JUL-1996
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REGISTRATION NUMBER: 24,618
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Result.

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                              91 ACCACCGCTGAACGTGAGATGGGAACAACATTTTCCTTGATAGCCGCTCTAGGCAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACAGCTG------GTTGGCCAGCTGCCATGGAGCACGGGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
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307 CTCAGCCAGGTCGTGGAGGAGGAGCAGGAAACCGAGGTGCCATCCAAGGGAGGATCC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TTCTACCCGGGGGGCCGCACCGCACCGCTGCAGCAAGGAGGATGGTGGGGGAACCTCTGTA 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 AAATGGTACTACCCAGACCAAACTTCTTCGCAACAGTCATGGCAAGGGCAACAAGGGTAC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 TyrTyrTyrProCysSerArgProGlyGluGlyTyrGlyTyrGlyGlnGlyGlyGlnArg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgMetArgCysCysCysGlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAla 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 TCAACTTTCCCG----CAGCAGCCAGGACAAGGACAA------CAACCAGGACAGGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LeuGinCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArgGlnValLeuAsp 54
                                                                                                                                                                                                                                                                                                                                                                               37 ATGGCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATC-----GTCGCCCTCGTGGCTCTC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 ArgGlnLeuThrGlyGlyGlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGly 74
                                                                                                                                                                                                                                                                                                                                                 1 MetalalysileAlaAlaAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal 20
                                                                                                                                                                                                                                                                                                                                                                                                           21 AlaValCysGlnGlyGluValGlu-------ArgGlnArgLeuArgAsp 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 Gln-----MetTyrPro-----ProCysArgProGlyThrThrGlyGly 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 IleArgSerMetValArgGlyTyrGluGlu-----
                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                    US-10-053-410-4 (1-206) x US-08-899-336-2 (1-2296)
                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08706391B
Patent No. 6174725
GENERAL INFORMATION:
APPLICANT: ANDERSON, OLIN D
REFERENCE/DOCKET NUMBER: 258
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 413-3200
TELEFAX: (703) 413-220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 base pairs
                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                          9.58e-14
281.50
46.12%
36.07%
24.52%
                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-706-391B-6
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101 GlyTyrGluGlu-----AlaMetProProLeuGluLysGlyTrpTrpProTrpGlyArg 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GinGinLeuGinAspValSerArgGiuCysArgCysAlaAlalleArgSerMetValArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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154 CAGTACGAACAGCAGATCGTTCTGCCCG-----AAAGGTGGTACCTTCTATCCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ValGinGluSerProLeuAspAlaCysArgGinValLeuAspArgGinLeuThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 cadcadcracerdacarcrcracadaraccaccaggrrgrrgrrcrccagrrgcragc
                                                                             ADDRESSEE: USDA, AGRICULTURAL RESEARCH SERVICE, PACIFIC
TITLE OF INVENTION: ALTERING DOUGH VISCOELASTICITY WITH MODIFIED GLUTENINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94710

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,391B
FILING DATE: 30-A09-1996
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: CONNOR, MARGARET A
REGISTRATION NUMBER: 30,043
REFERENCE/DOCKET NUMBER: 235.95/USDA96-001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
55
21
23
73
11
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-706-391B-6
                                                                                                                    STREET: 800 BUCHANAN STREET
CITY: ALBANY
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: ($10) 559-6067
TELEFAX: ($10) 559-5777
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 477 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0166
130.50
37.62%
27.23%
11.37%
                                           NUMBER OF SEQUENCES:
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I DZ A COMERA GA CE HI	Arighment Scores: Arighment Scores: All and Scores: Scores: Scores: All arity: All arity: All arity: All ariths: All ariths: Best Local Similarity: All ariths: Al
Db 268 AAGGCCTACTACTCGTCTGTTACTTGTCGCAGG	Alignment Scores:  0.0794

	Alignment Scores: Precal Smilarity: 124.00
Oy 116 TrpGlyArgGlnGlnGlnGlnProProProGlnGlyGlyGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	Mignment Scores   0.271   Length   1848   Escential Scores   124.00   Macches   65   Escent Scores   124.00   Macches   65   Escent Scores   124.00   Macches   65   Escent Scores   124.00   Macches   75   Escent Scores   10.804   Mismatches   75   Escent Scores   10.805   Mismatches   Mismatches   10.805   Mismatches   Mismat

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970 GGAGGTGCAGGCGGAGCTGGAGGACCTGGTGGAGCATACGGACCTGGTGGTGGATCATATGGA 1029
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                                                                                                  87 erArgGluCysArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGluAlaMetP 107
                                                                                                                                                                                                                                                                                                                                    --- GlnGlnPro 122
                                                                                                                                                                                                                                                                                                                                                                             921 ------AGGACCTGGTGGTGGTGGTGGACCTTACGGACCTGGCGGTTCTGGACCT 969
                                                                                                                                                                                                                                                                                                                                                                                                                        123 ProProGlnGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrProCysSerArgProGly 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GluglyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyrProProCysArgProGly 162
                                                                                                                                                      68 ProPheArgTrpGlyThrGly--LeuArgMetArgCysCysGlnGlnLeuGlnAspValS 87
                                                                                                                                                                                                    820 CCAGGAGGTGTAGGGCCTGGTGGCTCCGGACCAGGAGGTGTAGGACCTGGAGGTTCTGGA
                                                                    ---GlyGlyGlyGlyGlyGlyGlyValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
ATFLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
         107 roProLeuGluLysGlyTrpTrpProTrp-GlyArgGln----
                                                                                                                                                                                                                                                                                      880 ccaddaggreradaccrogregreregrecadaggagger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
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FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 ThrThrGly---GlyGlyPro 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08899595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                  52 ValLeuAspArgGlnLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6111072 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-899-595-4/c
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                                                                                                                                                                             476
619 ---GGCCGCCCTCGGCGATCCGCAGGCGGCGGTGCGCCGCGAGGCGGTGGCGGTGCTCGG 563
                                         132 GlyGlyTyrTyrTyrProCysSerArgProGlyGluGlyTyrGlyTyrGlyGlnGlyGly 151
                                                                      562 ------CTGGCTCCGCCACCAGCCGCCCTGGCCGA------ACTGGCCAGGCTGGC 518
                                                                                                                           152 GlnArgGlnMetTyrProProCysArgProGlyThrThrGlyGlyGlyProArgIleGly 171
                                                                                                                                                                           517 CAGCGCCGA-----TGTCGACCCGGAGGTACGCCGGGCGGCCACCGG----
                                                                                                                                                                                                                                               172 ArgValArg-LeuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCys 189
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: FALLS C......
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
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27
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-053-410-4 (1-206) x US-09-010-928B-3 (1-2824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09010928B Patent No. 5994099
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2824 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123.00
38.93%
32.21%
10.71%
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OTHER INFORMATION:
OTHER INFORMATION:
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US-09-010-928B-3
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32 LeuArgAspLeuGlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArgGln 51

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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 oCysSerArgProGlyGluGlyTyrGlyTyr------GlyGlnGlyGlyGlpAr 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LeuAspArgGlnLeuThrGlyGlyGlyGlyGlyGly------ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeu 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 ValAlavalAlavalCysGlnGlyGluValGluArgGlnArgLeuArgAspLeuGlnCys 37
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US-08-899-585-5
Sequence 5, Application US/08899595
Patent No. 6111072
GENERAL INFORMATION:
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE:
LENGTH: 5822 base pairs
                                                                                                                                                                                                                                                                                                                          43.09%
34.25%
10.32%
                      TYPE: nucleic acid_
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                          CDS
28..3972
                                                                                                                                  ORGANISM: Human
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Query Match:
DB:
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, LOCATION:
US-08-899-595-4
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3560 GGGGGGAATTCCAGCACTCCCAGGC-AAAGGAGGTGGTGGTGGGGGGGATTCTAGCACTC 3618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 GlnAspValSer-----ArgGluCysArgCysAlaAlaIleArgSerMet
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                                  STATE: D.C.
COUNTRY: USA
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
TIVING DATE: 24-UUL-1997
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62
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Mismatches:
Indels:
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Matches:
          3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         049441/0112
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REPREBINGE/DOCKET NUMBER: 0494
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 5822 base pairs TYPE: nucleic acid STRANDEDNESS: single
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43.09%
34.25%
10.32%
STREET: SUCTOTY: Washington
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT: MACC J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3022
                                                                                                                                                                                                                                                                              807 GCGCCACGCCCTGGACGATACCGAAATCCGCGCCCCATTCGCCGCGCTCGGCGTCGGCG 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 CGCCAGCGCCTGCGCCGCCGCGGAAGCGGCGGCGCGCAGGCGCTGGAAGCC 949
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                    ProProLeuGluLysGlyTrpTrpProTrpGlyArgGlnGlnGlnProProProGlnGly 126
                                                                                               GlyGlyGlyGlyGlnGlyGlyTyrTyrTyrProCysSerArgProGlyGluGlyTyrGly 146
                                                                                                                                    --GCTCGCCCAGCGCCAGCGCAGCT 776
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                                              147 TyrglyGlnGlyGlyGlnArgGlnMetTyrProProCysArgProGlyThrThrGlyGly
                                                                                                                                                                                                                 ------GGCGCGCGAACTGGC
                                                                                                                                                                                                                                                     167 GlyProArgIleGlyArgValArg------LeuThrLysAlaArgGluTyrAla
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                               777 GCAGGAAGCCGCGGC-----
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ORGANISM: Pseudomonas aeruginosa
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117.00
36.17%
28.19%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc O. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2647
LENGTH: 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identity of nucleotide at the above locations are unknown
---GGTGA 3782
                                                                                                                                                      ------GGAGGAGGAGGAGGAGTGGTACTATCCCCAGGAGCAGGTGGTGGTGG
                                                                                                                                                                                                                   3879 AATAATAGTGCCAGAGTCACCAGGTAAAGGAGGGGGCAGGGGGAACAGGAGCACGAGCTAGG 3938
                                                                                                                                                                                             171
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                                                                                                               137 oCysSerArgProGlyGluGlyTyrGlyTyr------GlyGlnGlyGlyGlnAr 153
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                                    gGlnGlnGlnGlnProPro---GlnGlyGlyGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrPr 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636 ceccédecececéchechechéceceacecececececéchhecececeange 695
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                                                                                                                                                                                          153 gGlnMetTyrPro----ProCysArgProGlyThrThrGlyGlyGlyGlyBroArgIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CAGCGCGCGAAGCTGGAGACCCTCGATCGGCAACTGCT-GGAGCAGGCGCAGACGATCAG
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                                                          3735 AGGAGGGGTGGAGATAGCAGTACCTCCAGGTAAAGAAGGG---
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-2647
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LOCATION: (58)
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US-09-252-991A-2647
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                                                                GlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCys
                                                                                                                                      -----GCTCGCCCAGCGCCAGGCT
                                                                                                                                                                                                        ------GGGGGGGGAACTGGC
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                                              ProProLeuGluLysGlyTrpTrpProTrpGlyArgGlnGlnGlnProProGlnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN;
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                        167 GlyproArgIleGlyArgValArg-
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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OTHER INFORMATION: represent a,
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SEQ ID NO 2
LENGTH: 4403765
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US-09-103-840A-2/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide at the above locations are unknown.
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                               665
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                                                                                                                                                                                         167 GlyProArgileGlyArgValArg------LeuThrLysAlaArgGluTyrAla 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 CysArg-----GlnValLeuAspArgGlnLeuThrGlyGlyGlyGlyGlyGlyGly 65
                   -caaggacgtactgaagagccggcgacgacgaggg
                                                           GlyGlyGlyGlyGlnGlyGlyTyrTyrTyrProCysSerArgProGlyGluGlyTyrGly
ProProLeuGluLysGlyTrpTrpProTrpGlyArgGlnGlnGlnProProProGlnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AladlyLeuProMetMetCysArg 190
                                                                                                                                                                                                                                                                                    541 CAAGGTGCGCCTGCGCCAGTACGT 518
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US-09-252-991A-2846
; Sequence 2846, Application US/09252991A
; Patent No. 6551796.
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ORGANISM: Pseudomonas
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2871151 CGTTTGCGACGTCCGGCAGCGCCAACTGGCTCACCCTGCCCGGGGGGGG	2 4 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	APPLICANT: TSUGAKI, Keiji APPLICANT: TSUGAKI, Keiji APPLICANT: KUBOTA, Michio APPLICANT: SUGINOTO, TOSHIJAUKI TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE NUMBER OF SEGURNCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: BROWDY AND NBIMARX STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/537,002A FILING DATE: 29-SEP-1995 CLASSIFICATION: 435	PRIOR APPLICATION DATA:  APPLICATION UNDHER:  FILING DATE: 01-00T-1994  PRIOR APPLICATION DATA:  APPLICATION NUMBER: JP No. 5773282 yet received  FILING DATE: 08-5EP-1995  ATTORNEY/AGENT INFORMATION:  REGISTRATION NUMBER: 25,618  REFERENCE/DOCKET NUMBER: TSUSAKI=1  TELECOMMUNICATION INFORMATION:  FILECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:	SEQ ID NO: 4: ACTERISTICS: Sel of a second and a second and a seco	Percent Similarity: 38.51% Conservative: 11 Best Local Similarity: 31.68% Mismatches: 56 Query Match: 10.15% Indels: 9 Bs: 10-053-410-4 (1-206) x US-08-537-002A-4 (1-2889)  Qy 55 ArgGlnLeuThrGlyGlyGly
2867371 TCACCGGGCTACCCGCCCCCCGCGAAGCGATGACTTGCGCGCTGGCCGCTTTTTTTT	OY 137 FIGURESCRIPTION OF THE CONTROL OF THE CONTRO	Db 2867143 CGCCTTGGCCGGGGTGTACCTGCTGGCTTGCCGC 2867099  RESULT 14 US-09-103-840A-1/C Sequence 1, Application US/09103840A Sequence 1, Application US/09103840A Sequence 1, Application US/09103840A Sequence 1, Application US/09103840A Sequence 1, Application US/09103840A APPLICANT: FRASER CIAire M. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: WHITE, OWEN R. APPLICANT R. A	ORGANISM: Mycobacterium tuberculosis   Order   Organism   Organi	SlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysCysCysCygGGGGTATG-CGGGCACCTTGGCCGCGATCCGGTGCTGT	2871

È	64	64 GlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGln 82
qq	2476	2476 GGAGGGGGAGCGCACCCCGAGGAGGGGACCAGGCTTCGGTCTCGTGCAGGGCCCCGG 2417
È	83	83 LeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValArgGlyTyr 102
QQ	2416	2416 GAAGGAGGCCTGGGGGTGCCCCCGGAGGCGGGAAGGCTTT 2366
ò	103	103 GluGluAlaMetProProLeuGluLys
qq	2365	2365 CCAGGAGCCGGACCTCCAGGGCGGAAGGTCCTGGGGGCGGCCGGGGGGGG
ò	115	115 ProTrpGlyArgGlnGlnGlnProProProGlnGlyGly 127
qq	2305	CCGTGAGGCCGAGGACCCTTCTGGAGGCGCCCCCGCTCCCAGAAGAGGCCCCCTTCGGGCC 2246
ò	128	
qa	2245	2245 GGAGAACCCAGGGGAGGTCCAGGCGGGGAGGACCCGCTCCGTGCGGTCCAGGCCCC 2189
ò	144	144 GlyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyrProCysArgProGlyThr 163
qa	2188	2188 CGTCTTGGACGAGGCGAGCTGGACCCACCCCTCCCCGCGCGAGTCCCG 2135
δ	164	164 ThrGlyGlyGlyProArglleGlyArgValArgLeuThrLysAlaArgGluTyrAlaAla 183
qa	2134	2134 GCCGGAGGACCTCCACGG
ò	184	184 Gly 184
qq	2092	2092 GGC 2090

Search completed: November 29, 2003, 19:16:29 Job time : 1629 secs

Human polynucleoti Sequence of the un Maize cinnamoyl Co Human cell growth, Human cell growth, DNA encoding novel Streptomyces nours

AAS85126 AAD17184

AAD17186

3147 65140 125401 6225 6225 6225 35384

Human cDNA differe Human signalling p Human immune/haema

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AAL40781 AAX09010

Oligonucleotide fo Oligonucleotide fo S. macromyceticus Human colon cancer

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DNA encoding novel DNA encoding novel Rabbit low density

AAA02484 AAS84408 AAS76210

1698 2049 2561

Human breast cance Human immune/haema

S.clavuligerus cla

ALIGNMENTS

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AAZ30700

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Gene expression regulatory DNA, expression cassettes and vectors - comprising promoter region from barley, Hordeum vulgare, D-hordein
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                           AAV20662;
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Barley CDNA involv
Barley CDNA involv
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Human low density
Human low density
HSV-2 immediate ea
HSV-2 immediate ea
Human herpesvirus
                                                                                                    November 29, 2003, 13:23:43 ; Search time 317 Seconds (without alignments) 8089.799 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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| SIDSI/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseqn-embl/NA1991.
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                                                                                                                                                                                                      950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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           5.1.6
Compugen Ltd.
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             version 5
- 2003 C
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Maximum Match 100%
Listing first 45 summaries
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AAF63380
AAF63379
AAX53491
AAH26499
AAH26495
AAA09686
                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
             GenCore (c) 1993
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seq length: 200000000
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Maximum DB
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Kuroda H; Hirota N, Ito K, Kihara M, 96JP-0193433. 97WO-JP02526 SAPB ) SAPPORO BREWERIES WPI; 1998-120779/11. Hordeum vulgare. 23-JUL-1996; 22-JUL-1997; WO9803655-A2 29-JAN-1998.

us-10-053-410-3.rng

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Hirota N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the 5'-terminal region of the barley D-hordein gene. The present invention describes gene expression D-hordein gene. The present invention describes gene expression cregulatory DNA which comprises a promoter region derived from the barley (Hordeum vulgare) D-hordein gene which allows expression of a dealred structural gene, and a regulatory region regulatory cassettes containing the gene expression regulatory DNA (either directly or via expression vectors) enables the expression of a gene within a plant cell e.g. barley to be controlled. The use of activating and suppressing cegions in the regulatory DNA allows control of expression by e.g. tissue type or developmental stage, whilst huse of only an activating region maintains expression at a high level, providing an effective production means when recovery of the product of the structural gene is greduction means when recovery of the product of the structural gene is production means when recovery of the product of the structural gene is greducting seed endosperm tissue or regeneratable plant cells (e.g. derived from anthers) to improve seeds of barley or other plants, to produce gene products in seeds or to contribute to plant breeding programmes. The expression regulatory DNA can also used in expression systems in the expression regulatory ball and also the promoter region was 1.5 times below the product of the product region main promoter region was 1.5 times below the product of the product of the product region product region product region was 1.5 times below the plant of the product of the product region was 1.5 times the product of the product of the product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region product region pro
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expression of desired gene e.g. to improve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91.2; DB 19; Length 2296;
Pred. No. 2.6e-07;
0; Mismatches 88; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2296 BP; 629 A; 708 C; 606 G; 353 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barley cDNA involved in D-hordein production SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              higher than in those transfected with control pACT1F.
                                                    Example 3; Page 25-26; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.4%;
Matches 178; Conservative
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 useful to control
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                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to barley having a low gel protein content. The barley is transformed with a polynucleotide sequence which regulated the formation of D-hordein. Transformation results in the production of barley strains with improved malting properties such as wort filterability and efficiency of extraction. The present sequence represents cDNA involved in the regulation of D-hordein production.
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                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 33-34; 40pp; Japanese.
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                                                              (SAPB ) SAPPORO BREWERIES LTD
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99JP-0229696.
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Matches 178, Conservative
                                                                                                                                 Kihara M,
                                                                                                                                                                                                WPI; 2001-191587/19.
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16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                    ACGGGGCTCCAGATGCAGTGCTGCCAGCTTCGGGACGTCAGCCCCGAGTGCCGCCCC 300
                                                                                                                                                                                                                                                                                                                                                                                                            GCCGCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCATGCCGCCGCTGGAGAAAGGC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gredecerchadecadereradecaaraceadecadeaaaceaderecarecaadeea 360
                                                                                          This invention relates to barley having a low gel protein content. The barley is transformed with a polynucleotide sequence which regulated the formation of D-hordein. Transformation results in the production of barley strains with improved malting properties such as wort filterability and efficiency of extraction. The present sequence répresents cDNA involved in the regulation of D-hordein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                          267 CTCGACCGGCAGCTAACCGGCGGCGGCGGCGGCGGCGGCGTTGGCCCGTTCCGGTGGGGC
                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary vasoconstriction; emphysema; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                          207 AGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGCCCGCTCGACGCGTGCCGCCAGGTC
                                                                                                                                                                                                                                   Gaps
                                 Transformation of barley with a D-hordein expression regulator for production of barley with lowered gel protein content
                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 GGATCCTTCTACCCGGGCGGGACCGCACCGCCGCTGCAGCAAGGAGGATG 410
                                                                                                                                                                                                           DB 22; Length 2434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenosine Al receptor antisense oligonucleotide fragment
                                                                                                                                                                                                                                   88; Indels
                                                                                                                                                                                   Sequence 2434 BP; 675 A; 757 C; 626 G; 376 T; 0 other;
                                                                                                                                                                                                          Score 91.2; DB 2;
Pred. No. 2.6e-07
                                                                                                                                                                                                                                  0; Mismatches
                                                                      Claim 4; Page 31-33; 40pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX53491 standard; DNA; 114955
                                                                                                                                                                                                           9.6%;
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97US-0059160.
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non-coding regions of RNAs corresponding to target genes, gene initiation codons, genemic flanking regions, intron-exon borders, the conditions and all segments of RNAs encoding proteins associated with one regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides corresponding to the conditions of a mixtures. The antisense oligonucleotides (appecifically AAX55272-74) can be used for the conditions are those associated with impaired respiration and conditions. Typical diseases and conditions are those associated with impaired respiration and condition, including lung diseases, pulmonary vasoconstriction, including lung diseases, pulmonary vasoconstriction, crepiration, raspiratory distress syndrome, pain, cystic fibrosis, culmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, arctionems e.g. colon cancer, breast cancer, lung ancert, melanoma, partic metastases, as well as all types of cancers which may metastasize hepatic metastasize as a large of cancers which may metastasize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108383 CCSNNNDNNGGCGGGGGCGCGCGCCTGGCTCGCSNNNDNNGGCGGGGGCGCGCGCGCC 108442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108498 GCGCCCTGGCTSNNNDNNGGCGGGGGGGGGGGCGCCTGGCSNNNDNNGGCGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
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                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 37; 120pp; English.
(UYEC-) UNIV EAST CAROLINA
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                                                                                               168 GTGGCCGTCTGCCAAGGCGAGGTCGAGCGGCAGAGGCTCAGGGACCTGCAGTGCTGGCAG
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  108854 CGCCTGGCTCGCCTBGGGCCCCSNNNDNNGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCC 108913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the coding region of the human gene (see also AAH26494) encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA library using LBP-2 CDNA as probe. The LBP-2 protein predicted from the present sequence differs from that the contains an additional 32 mains each as ABB2803) in that it contains an additional 32 mains ocids at its N-terminus (the cDNA is a 5 truncation). LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed.

Characterical compositions, are also claimed.
                                                662 GITGCCGATGATGTGCCGGCTGTCGGAGCCCCAGGAGTGCAGCATCTTCTCCGGCGCGCGA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human low density lipoprotein binding protein 2 (LBP-2) DNA
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                                                                                                                                                                                                                                                                                                              AAH26499 standard; DNA; 1614 BP.
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14-JUL-2000; 2000US-0616289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of genomic DNA encoding novel human conditions of the DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The Open reading frame spans 5 exons. Human LBP-2 cnucleic acids are among claimed polynucleotides of the Tivention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Ale ragments and analogues cof them, as well as expression vectors, cells and methods of producing the LBPs. Methods for evaluating an agent for use in abnormality in structure or metabolism of LBP and methods of treating atherosclerosis, and methods for evaluating an agent for use in abnormality in structure or metabolism of LBP sure claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 GIGGCCGTCTGCCAAGGCGAGGTCGAGGCAGGCTCAGGGACCTGCAGTGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 AGGGGCTACGAGGAGGCCATGCCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGGCGGCAG
                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 GAGGICCAGGAGACCCGCTCGACGCGTGCCCCAGGICCTCGACCGGCAGCTAACCGGC
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                                                                                                                  Law SW, Arjona AA;
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                                                                                           (BOST-) BOSTON HEART FOUND INC
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Best Local Similarity 46.4%;
                                                         2000US-0517849
2000US-0616289
                                  28-FEB-2001; 2001WO-US06356
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                                                                                                                                       WPI; 2001-565505/63.
P-PSDB; AAB82806.
                                                                                                                  Lees RS,
                                                         32-MAR-2000;
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            07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to an immediate early herpes-simplex-virus type 2 (HSV-2) infected cell protein 4 (ICP4) recognised by human cytotoxic T cells. HSV-2 ICP4 protein is recognised by cytotoxic T-lymphocyte (CTL) cells in humans and is used in vaccines for therapeutically or prophylactically treating HSV infections. Pharmaceutical compositions of HSV-2 ICP4 protein may be used to treat patients suffering from HSV infections, to prevent or decrease recurrent herpes disease, frequency, severity and duration of episodes. The present sequence represents HSV-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immediate early herpes-simplex-virus type 2 (HSV-2) ICP4 protein is used in vaccines for therapeutically or prophylactically treating HSV
                                                                                                                                                                                                                                                            Herpes-simplex-virus type 2; HSV-2; infected cell protein 4; ICP4; vaccine; infection; ds.
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45.8%; Pred. No. 0.021;
tive .0; Mismatches 301;
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AAA09686 standard; DNA; 3957 BP
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487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compaired not oral delivery of vaccines, comprises expression vector containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension
                                                         CTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGTCCCCGGCACCACCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                      608 CGGGCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCGGGAGTACGCCGGGGGTTGCC
GCCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGGCGGCGAGCAGCAGCCGCCGCCGCAGGG
                                                                                                                            488 AGGAGGAGGAGGACAGGGGGGTACTACTACCCCTGCAGCCGGCCAGGAGAGGGATACGG
                                                                                                                                                                                                                                                                                                                      Human herpesvirus 2 complete DNA genome.
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contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or different promoter polynucleotide sequences. The expression vector, as a DNA vaccine is useful for treating a condition in an organism. The present sequence is human herpesvirus 2 complete DNA genome related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GGGGGGGGGGGGGGGGGTGTGGCGGCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGA
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                                                                                                                                                                                                                                                                                 Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                            Score 63.4; DB 24;
Pred. No. 0.027;
0; Mismatches 301;
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Matches 259; Conservative
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   608 CGGGCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCGGGGAGTACGCCGCGGGGTTGCC
                                                             CTACGGTCAGGGTGGCCAGCGCAGATGTATCCACCGTGTCGTCCCGGCACCACCGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product= "Protein of ORF 5"
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product= "Protein of ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (7703..6693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9464..8130)
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                                                                                                                                                                                                                                                                                               668 GATGATGTGCCGGCTGTCGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL40781 standard; DNA; 88421 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152116 GCGGCGCCCTGGCCGGGGCGGGCTCTTGCGCGTTGCGCGCCTCCCGCGGGGGCGCGAAGGCGG 152057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or different promoter polynucleotide sequences. The expression vector, as a DNA vaccine is useful for transfing a condition in an organism. The present sequence is human herpesvirus 2 complete DNA genome related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCGAGCGGCAGAGGCTCAGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGAGCCCGCT 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCCGCGAGTGCCGCTGCGCCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCAT 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition comprising an expression vector bound to an aggregated protein-polycationic polymer conjugate or buspension. The expression vector contains a promoter polynucleotide sequence expression vector contains a promoter polynucleotide sequence operatively linked to a polynucleotide sequence encoding an antigen which is a fragment of a gene or genome associated with an infectious disease, cancer and autoimmune disease such as rheumatoid arthritis, vasculitis, and multiple sclerosis, pathogenic genomes consisting of bacterium, fungus, protozoa and virus such as human immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C virus (HCV), infihenza and respiratory syncytial virus (RSV), and optionally comprising a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response of systemic and/or mucosal) in an organism. The cytokine expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGGCGCGCGCGCTGTGCTTCGCGGCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGA 187
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Pred. No. 0.027;
0; Mismatches 301; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 90-132; 145pp; English.
                                                                                                                                                                                                                                                                                               Bhogal BS;
                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                 06-APR-2001; 2001WO-US11372.
                                                                                                                                                                           07-APR-2000; 2000US-195680P
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                                                                                                                                                                                                                                                                                               Orson FM, Kinsey BM,
                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-066308/09.
WO200176643-A1
                                                       18-OCT-2001.
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us-10-053-410-3.rng

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ORF

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product= "Protein of ORF 22"
5535..76464
*tag= w
                                                                                                                                                /product= "Protein of ORF 20"
complement (74216..73563)
                                                                                                                                                                       /product= "Protein of ORF 21"
complement (75424..74213)
                                                                          product= "Protein of ORF 17"
0099..70662
*tag= r
                                                                                                                                                                                                                     /product= "Protein of ORF 23"
complement (78110..76449)
                                                                                                                                                                                                                                            product= "Protein of ORF 24"
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complement (81624..79861)
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84481. 85548
                                                                                                                                                                                                                                                                                                                                        product= "Protein of ORF 28"
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'product= "Protein of ORF
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85556..86845
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97372 .86803
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                                                                                                                                 complement (73439..71964)
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                           /product= "Protein of
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87494..88420
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              55826..66530
                                                           57384..70059
                                                                                                           0659..71906
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/*tag≈ ac
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12-APR-2001; 2001US-283296P.
24-JUL-2001; 2001US-0910813.
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The invertion relates to an isolated ramoplanin blosyntheeit pathway polypeptide aelected from a polypeptide of open reading frames (ORF) (CC 1-32. The isolated polypeptides are useful for chemically modifying a campolanin biosynthesis gene cluster, by contacting the biological molecule that is a substrate for a polypeptide encoded by a ramoplanin biosynthesis gene cluster, by contacting the biological molecule. The method comprises contacting the biological molecule. The method comprises contacting the biological molecule. The method comprises contacting the biological molecule. The method comprises contacting the biological molecule with at least two different polypeptides encoded by campolanin ORFs 1-31. The polypeptides are useful for directing the biological antibiotic ramoplanin in microorganisms. An isolated comprising the ORFs is useful as a substrate for concomplating nucleic acid sequence is useful for generating derivatives of cramoplanin, for improving production or for producing variants of cher antibiotics of the peptide class. The isolated polypeptides are useful controporation of Thr into a peptide antibiotic precursor, for modifying catcher and/or enhancing fatty acid structure and/or enhancing secretion of campolanin or its variants and derivatives, for chancing upcake of the peptide antibiotic, for enhancing production of a ramoplanin products or its variants and derivatives, for chancing preduction of cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or derivatives, to cramoplanin products or its variants or d 243 ccecriceacecerecceccaegricorceaegacaecraace--eceeceeceece 183 GGCGAGGTCGAGCGCGAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGAGAGC Novel isolated ramoplanin biosynthetic pathway polypeptide useful for chemically modifying biological molecule that is a substrate for a polypeptide encoded by a ramoplanin biosynthesis gene cluster -P-PSDB; AA022146, AA022147, AA022148, AA022149, AA022150, AA022151, AA022152, AA022153, AA022153, AA022154, AA022155, AA022156, AA022156, AA022158, AA022165, AA022165, AA022165, AA022165, AA022165, AA022165, AA022165, AA022167, AA022167, AA022167, AA022167, AA022167, AA022167, AA022167, AA022167, AA022167, AA022167, AA022172, AA022172, AA022173 Gaps The invention relates to an isolated ramoplanin biosynthetic pathway 5; Sequence 88421 BP; 10639 A; 32391 C; 32663 G; 12728 T; 0 other; Query Match 6.6%; Score 63; DB 24; Length 88421; Best Local Similarity 54.6%; Pred. No. 0.031; Matches 147; Conservative 0; Mismatches 120; Indels 2. Disclosure; Page 87-135; 212pp; English. microorganism of the invention. 2002-435445/46 ઠે 유 ઠે g

RESULT 11 AAX09010

us-10-053-410-3.rng

Gaps

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AAX09010 standard; cDNA; 1272 BP
                                                             Latchman DS,
       14-JUN-1999
                             Homo sapiens
                                         WO9905272-A1
                                                17-JUL-1998;
                                                    10-DEC-1997;
                                                      25-JUL-1997;
                                             04-FEB-1999.
   AAX09010
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WO200034466-A1
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                                                         Brn-3a, Bcl-2, neurons, neuronal cells, apoptosis, cell death, CNS, PNS, central nervous system, parasympathetic nervous system, development, injury, neurotrophic factor; nerve growth factor; NGF, ciliary neurotrophic factor, CNTF, brain-derived neurotrophic factor, BNTF, neurodegenerative disease; familial dysautonomia, infantile muscular dystrophy; Parkinson's disease; Alzheimer's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising transcription factor Brn-3a, or its derivative - useful for treating nervous system diseases, preventing cellular apoptosis and increasing nerve regeneration following neuronal damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuronal cell death and/or lack of nerve regeneration, especially neurodegenerative diseases such as familial dysautonomia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infantile muscular dystrophy, and Parkinson's and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1272 BP; 202 A; 468 C; 452 G; 150 T; 0 other;
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/product= Brn_3a_polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 61-62; 68pp; English.
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Brn-3a polynucleotide
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20; Length 1272;

Score 62.4; DB Pred. No. 0.03;

6.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 GGGGCACCGGGCTCCGGATGCGGTGCTGCCAGCAGCTCCAGGACGTGAGCCGCGAGTGCC 381
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HPV; antisense; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Product for treating, preventing and diagnosing cervical cancer comprises a nucleotide sequence or molecule which binds to Brn-1 decreases its intracellular levels or inhibits its activity
5;
0; Mismatches 196; Indels
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Matches 192; Conservative
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P-PSDB; AAY96404.
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98WO-US19419

17-SEP-1998;

25-MAR-1999

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A product that binds, causes a decrease in intracellular levels of or inhibits the activity of Brn-3a useful for treating, prevention or diagnosis of cervical cancer caused by human papilloma virus (HPV) is claimed. Expression of HPV proteins is generally dependent on the presence of Brn-3a in the cell. Methods of identifying Brn-3a binding agents or agents which inhibit Brn-3a expression are claimed. Nude mice were injected with Sida cells containing a single integrated HPV16-genome were transformed with a Brn-3a antisense construct and with the empty expression vector as control and tumours assessed at regular intervals. Results showed that after 30 days there was no or very little tumour
                                                                                                                                                                                                                                                                                                              growth in mice transformed with Brn-3a antisense construct as compared
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Seguence 1272 BP; 202 A; 468 C; 452 G; 150 T; 0 other;

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Score 62.4; DB 21; Length 1272; Pred. No. 0.03;
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Human adenosine Al receptor antisense oligonucleotide fragment AAX53491 standard; DNA; 114955 05-JUL-1999 (first entry) 

impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy, asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemis; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis; Antisense oligonucleotide; multiple target; antisense treatment; prostate cancer; ss.

WO9913886-A1 Synthetic

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110308 GCGGCGCGCGCGCGCC-CCNNHNNNSGCGGCGCGCGCGCGCGCCCCNNHNNNSGCCACG 110250
                                                                               417 GAGGAGGCCATGCCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGGCGGCAGCAGCAGCCG
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directed against at least 2 mRNAs selected from target genes, coding and directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, genee, controlled and and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one compared from sequences ArX55272-74. These multiple target may be derived from sequences ArX55272-74. These multiple target oligonucleotides (specifically AAX5580-271) can be used for the conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, including lung diseases, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary diseases (COPD), and cancers such as leukemias, increase compared and concers such as leukemias, increase. 110548 GGGGNNHNNNSGGCGGGGGGGGCGCGCCNHNNNSGGCGGGCGGCGCGGGGCCCNNHNNNS 110489 110668 CNNHNNNSGGCGGGCGCGNNHNNNSGGCGGCGCGCGCNNHNNNSGGCGGGCGCGCGCNN 110609 110488 GGCGGGCGCGCGGGGGCCCNNHNNNSGCGGGGGCCCCNNHNNNSGGCGCGGGGCCCCNN 110429 110428 HNNNSCGGCGGGGCCCCNNHNNNSGCGGCGCGGGGCCCCNNHNNNSGCGGGGGGGGG 110369 416 lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer. CAAGTGGCGACAGACAAGATTTGTGAGGGTGATCCGCGCTGAGAAGAGAGATTGGCTAAGAT 182 AGGCGAGGTCGAGCGGCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGAGAG --- GGCGGCGTTGGCCCGTTCCGGTGGGCCACCGGGCTCCGGATGCGGTGCTGCCAGCAG CTCCAGGACGTGAGCCGCGGGGGCTGCGCCCCCATCCGGAGCATGGTCAGGGCCTAC 8; Gaps New antisense oligonucleotides used in treatment of, e.g. pulmonary Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other; Query Match 6.5%; Score 61.6; DB 20; Length 114955; Best Local Similarity 32.9%; Pred. No. 0.055; Matches 221; Conservative 59; Mismatches 384; Indels 8; Disclosure; Page 37; 120pp; English. 98US-0093972. UYEC-) UNIV EAST CAROLINA WPI; 1999-229400/19 vasoconstriction 09-JUN-1998; 17-SEP-1997; 300 62 357 Nyce JW; 셤 g 셤 셤 ઠે ઠે ઠે ò ሯ

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                                                                                                                110131 CGAGCVCVVNNHNNNSGCCACGACGAGCVCVVCNNHNNNSGCCACGACGAGCVCVVCGNN 110072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                     ACCACCGCCGCCGCCCAAGGATCGGCCCCGTGAGGCTTACGAAGGCCCCGGGAGTACGCC
                                       110249 ACGANNHNNNSGCCACGACGAGNNHNNNS--GCCACGACGAGCNNHNNNSGCCACGACGA
CCGCCGCAGGGAGGAGGACAGGGGGCTACTACTACTACCCCCTGCAGCCGGCCAGGA
                                                                                   GAGGGATACGGCTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGTCCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J, Innis MA, Garcia PD, Sudduth-Klinger Randazzo F, Kennedy GC, Pot D, Kassam A, Crkvenjakov R, Dickson M, Dranane S, Lab Garcia V, Jones LW, Stache-Crain B;
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Randazzo F,
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98US-0085537.
98US-0085696.
98US-0105234.
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCACCACCGCGGCGGGCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCGGGAGTA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1053
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The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, oestrogen receptor-negative breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60; DB 21; Length 1127; Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 374; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1127 BP; 3 A; 214 C; 505 G; 49 T; 356 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%;
Best Local Similarity 36.2%;
Matches 216; Conservative
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145 TGTGCTTCGCGGCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGAGGTCGAGCGGCAGAGGC 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTCGACCGGCAGCTAACCGGCGGCGGCGGCGCGCGGCGTTGGCCCCGTTCCGGTGGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIAX DP2-64 (Oct-T1) gene. The protein is a tumour rejection antigen precursor (TRAP). The specification describes the treatment of disorders which characterised by expression of a leukaemia-associated nucleic acid such as TRH. The products are used for in vivo or in vitro screening for leukaemia, lymphoma or other cancers by usual hybridisation/amplification or immunoassay methods. TRAPs, when processed to antigens or complexed with High (human lymphocyte antigen) molecules, or nucleic acid encoding them, are useful in vaccines for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  refectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedesectedes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnosis of leukaemia - by detecting genes for tumour antigen rejection precursors or corresponding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Baren N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the nucleotide sequence of the SIAX DP2-64 (Oct-T1) gene. The protein is a tumour rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3%; Score 59.4; DB 20; Length 4524; 48.8%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4524 BP; 1177 A; 1090 C; 1180 G; 1077 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lucas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caecarecaecaecarcecececes 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Smet C,
Location/Qualifiers
174..1436
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Pages 63-67; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                   97US-0845998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 48.8 Matches 189; Conservative
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treating leukaemia.
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                                                                                                                                          WO9849299-A1
                                                                                                                                                                                                                                                                       22-APR-1998;
                                                                                                                                                                                                                                                                                                                                       25-APR-1997;
                                                                                                                                                                                                   05-NOV-1998.
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Search completed: November 29, 2003, 14:10:55 Job time: 323 secs

Sequence 1, Appli Sequence 1142, Ap Sequence 3559, Ap Sequence 3557, Ap Sequence 14511, A

Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

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Sequence 2, Application US/08899336

Patent No. 595549

GENERAL INPORMATION:
APPLICANT: KIHARA, MAKOTO
APPLICANT: KUHARA, HISOO
APPLICANT: ITO, KAZUTOGHI
TITLE OF INVENTION: EXPRESSION REGULATORY DNA,
TITLE OF INVENTION: EXPRESSION CASSETTE, EXPRESSION VECTOR AND TRANSGENIC
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: END PY Compatible
COMPUTER: Floppy disk
COMPUTER: END PY Compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,336
FILING DATE: 23-JUL-1997
CLLASSIFICATION: DATA:
APPLICATION NUMBER: JP HEI 8-193433
FILING DATE: 23-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NUMBER: 24-618
REFERENCE/DOCKET NUMBER: 2599-0061-0
TELEFRANCE/DOCKET NUMBER: 2589-0061-0
                                                                                                  US-09-252-991A-1142
US-09-252-991A-3549
US-09-252-991A-357
US-09-252-991A-14511
US-09-252-991A-14511
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-09-252-991A-3346
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: double
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ZIP: 22202
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Sequence 14814, A
Sequence 7125, Ap
Sequence 15075, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Appli
Sequence 1153, Ap
Sequence 713, App
Sequence 1, Appli
Sequence 3, Appli
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Sequence 14293, A
Sequence 14262, A
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Sequence 15328, A
Sequence 1104, Ap
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Sequence 16, Appl
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5590.853 Million cell updates/sec
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                                                                                                                                                                                                                                                                                       November 29, 2003, 14:01:53; Search time 75 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-14411
US-09-252-991A-14235
US-09-252-991A-14223
US-09-252-991A-14223
US-09-252-991A-14262
US-09-252-991A-14814
US-09-252-991A-1125
US-09-252-991A-1125
US-09-252-991A-1125
US-09-252-991A-1055
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US-09-252-991A-1104
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US-09-430-854-7
US-09-016-434-1153
US-09-620-312D-713
US-08-924-345-1
US-09-043-937A-3
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US-09-103-840A-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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61.4%; Pred. No. 8.2e-09;
iive 0; Mismatches 88; Indels
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ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsteardam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7008
TELECOMMUNICATION:
TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Van Baren, Nicolas APPLICANT: Coulie, Pierre G. APPLICANT: De Smet, Charles APPLICANT: Lucas, Sophie APPLICANT: Boon, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Best Local Similarity 61.4
Matches 178; Conservative
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-845-998-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 GCACCGGGCTCCGGATGCGGTGCTGCCAGCAGCTCCAGGACGTGAGCCGCGAGTGCCGCT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     712 degecédecretendes de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contracted de contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 TGTGCTTCGCGGCCCTGGTGGCCGTCGCCAAGGCGAGGTCGAGCGGCAGGC
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Score 59.4; DB 2; Length 4524;
Pred. No. 0.0072;
0; Mismatches 196; Indels 2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Boon, THIEBERTY
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolf, Greenfield & Sacks, P.C.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
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Patent No. 6130052
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(617)720-2441
        Query Match
Best Local Similarity 48.8<sup>1</sup>
Matches 189; Conservative
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ADDRESSEE: Wolf, Green
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MEDIUM TYPE: Floppy
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STREET: DOTATION
TITY: BOBTON
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145 TGTGCTTCGCGGCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGAGGTCGAGCGCGGCAGAGGC 204
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Pred. No. 0.0072;
0; Mismatches 196; Indels
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECT:
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                 08/845,998
                                                                                                        FILING LDAIE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 100461
TELECHONE: (617)720-3500
TELEPHONE: (617)720-341
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LINGARA 4524 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.8%;
Matches 189; Conservative
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STRANDEDNESS: double
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174..1433
         PRIOR APPLICATION DATA:
                                                 APPLICATION NUMBER:
FILING DATE:
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STATE: CALIFORN
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FEATURE:
NAME/KEY: CDS
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US-09-430-854-7
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Pred. No. 0.0072;
0; Mismatches 196; Indels 2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolf, Greenfield & Sacks, P.C.
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Patent No. 6271019
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APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
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STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.8*;
Matches 189; Conservative
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4524 base pairs
                                                 nucleic acid
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174..1433
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                                                                                                                                                linear
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                                                      TYPE: nucleio
STRANDEDNESS:
                                                                                                                                           TOPOLOGY: 1i:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ns
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                                                                                                                                                                                                                                                                                  ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-206-537-7
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US-09-430-854-7
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591 264 711

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APPLICANT:
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: POLYpeptides
TITLE OF INVENTION: POLYpeptides
TITLE OF INVENTION: POLYpeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT PILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL-Lgenes Version 1.0
SQL ID NO 713
LENGTH: 3169
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Best Local Similarity 52.2%; Pred. No. 0.0083;
Matches 131; Conservative 0; Mismatches 120; Indels
                             COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION NATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASIFICATION:
ATTORNEY FAGNT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-0456
INFORMATION FOR SEQ ID NO: 1153:
SEQUENCE CHARACTERISTICS:
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US-09-620-312D-713/c
; Sequence 713, Application US/09620312D
; Patent No. 6569662
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: 1ang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Agundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
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CLONE: 91524108
US-09-016-434-1153
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182 AGGCGAGGTCGAGCGCCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGAG 241
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                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                     Score 57.4; DB 4; Length 3169;
Pred. No. 0.016;
0; Mismatches 211; Indels 1
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Sequence 1, Application US/08924345
Patent No. 6224878
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
APPLICANT: AUDONNET Jean-Christophe, Francis
APPLICANT: AUDONNET Jean-Christophe, Francis
APPLICANT: AUDONNET Jean-Christophe, Francis
APPLICANT: MUDANTION: Mutants and vaccines of the Infectious
TITLE OF INVENTION: Bovine Rhinotracheitis virus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: LARSON AND TAYLOR
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.9%;
Matches 195; Conservative
                                                                                         ; NAME/KEY: CDS
; LOCATION: (116)..(2146)
US-09-620-312D-713
TYPE: DNA ORGANISM: Homo sapiens
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Xue, Aidong J. Yang, Yonghong Wang, Jian-Rui

Qing A.

Wehrman,

Zhao,

APPLICANT: APPLICANT:

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NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1487-20 TELECOMMUNICATION INFORMATION:
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LOCATION: 195..1310
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
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STRANDEDNESS: double
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LOCATION: 172..1311
LOCATION: 172..1311
OTHER INFORMATION: /function= "envelope glycoprotein"
OTHER INFORMATION: /function= "glycoprotein gl"
OTHER INFORMATION: /fundard_name= "BHV-1 gl"
FRATURE:
FRATURE:
LOCATION: 1594..3318
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OTHER INFORMATION: /product= "glycoprotein gE"
OTHER INFORMATION: /standard_name= "BHV-1 gE"
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,345
FILING DATE: 04-28P-1997
CLASSIFICATION: 424
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; COTHER INFORMATION: /product= "protein US9"
COTHER INFORMATION: /standard_name= "BHV US9"
US-08-924-345-1
727 SOUTH TWENTY-THIRD STREET
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ORIGINAL SOURCE:
ORGANISM: Type 1 Bovine Herpesvirus
STRAIN: ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,172
FILING DATE: 09-AUG-1994
APPLICATION NUMBER: FR 92 07930
FILING DATE: 26-UUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SARRO, THOMAS P.
REGISSTRATION NUMBER: 19396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: L. REGISTRATION NUMBER: XI TELECOMUMICATION INFORMATION: TELEPHONE: (703) 920-7200 . TELEFAX: (703) 892-8428 . INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4190 base pairs TYPE: nucleic acid cTRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
NNTF CHETICAL: NO
                                                       CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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Sequence 3, Application US/09043937A

Sequence 3, Application US/09043937A

Patent No. 6211432

GENERAL INFORMATION:

APPLICANT: BOUDET, ALAIN-MICHEL

BICHON, MAGALIE

GRIMA-PETTEMATI, JACQUELINE

BECKERT:

GAMAS, PASCAL

GAMAS, PASCAL

BRIAT, JEAN-FRANCOIS

TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-COA

LIGNIN CONTENTS IN PLANTS

LIGNIN CONTENTS IN PLANTS
                                                               369 AGCCGCGAGTGCCGCTGCGCCGCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCATG 428
                                                                                                                     921 AAACGCCGAGCCCGCCTCCTCGCGGCCTCGACTTCCGTCGTCGTCGACCCTCTCTGG 862
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429 CCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGGCGGCAGCAGCAGCCGCCGCCGCCGCAGGGA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-Jul-1998
CLASSIFCATION: «UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/FR96/01544
FILING DATE: 03-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: SADOPF, B.J.
RESISTRATION NUMBER: 36.663
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3941454 CAACGCTCCGGCGGCGCCGCGCACTGGCGGACAAGGCGGCGCCGGGGGTGCTGGCGG 3941513
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                                                                                                                                      3941514 GGCCGGCGCCGATAACCCCACCGGCATCGGCGCCACCGGCGGCGCGCGGCGGCGCACCGGCGG
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Pred. No. 0.09;
0; Mismatches 235; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PELLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO I.
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3941754 TGGAGCCGGCGGGCCCGCGG 3941774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
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ilarity 47.9%;
Conservative
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Best Local Similarity
Matches 218; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-840A-1
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Bacent No. 6294328

GENERAL INFORMATION:

APPLICANT: FLEISCHAMN, Robert D.

APPLICANT: FRASEX:

APPLICANT: FRASEX:

APPLICANT: WHITE, Owen R.

APPLICANT: WITE, Owen R.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT PILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGCAGGAGGTCCAGGAGGCCCGCTCGACGCGTGCCGCCAGGTCCTCGACCGGCAGCT
                                                                                                                                         101 CTGAGAAGAGATGGCTAAGATCGCCGCGGCGGCGGCGGCGGCGCCTTTCGCGGCCCT
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5.8%; Score 55.4; DB 3; Length 4403765;
Best Local Similarity 45.9%; Pred. No. 0.076;
Matches 230; Conservative 0; Mismatches 266; Indels 5;
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OTHER INFORMATION: "n" bases at various positions throughout the
OTHER INFORMATION: represent a, t, c or g
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   Score 56.4; DB 3; Length 1556;
Pred. No. 0.024;
0; Mismatches 166; Indels 0
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Query Match 5.9%;
Best Local Similarity 48.4%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4403765
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US-09-103-840A-2
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                                      Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
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Application US/09252991A
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 48.1%;
Matches 150; Conservative
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APPLICANT: Weissman, Namadev
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
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COMPUTER TREADABLE FORM:

COMPUTER: Floppy disk

COMPUTER: BM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NATH.

APPLICATION NUMBER: US/08/758,662

FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                             533 AGGAGAGATACGGCTACGGTCAGGGTGGCCAGC 567
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6114150tenburg Ph.D., Carol
RESISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 390036.402C1
TELECOMMUNICATION INFORMATION:
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Gaps

261

321

5.6%; Score 52.8; DB 4; Length 888; 48.1%; Pred. No. 0.11;

Query Match Best Local Similarity

RESULT 12 US-09-252-991A-14411/c

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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OS 60/094,190

RION PILING DATE: 1998-07-27

NUMBER: OS 60/094,190

ERIOR FILING DATE: 1998-07-27

NUMBER: OS 01 D NOS: 33142

SEQ 1D NO 14293
395 CCGGAGCATGGTCAGGGGCTACGAGGAGCCCATGCCGCCGCTGGAGAAAGGCTGGTGGCG 454
                                                                  417 CGCGGCGATCCTCGAGGCCTACGGCCTCGACGTAACCTACCCTGAACAGGGCGACGACGACA 476
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                                                                                                                                            455 ATGGGGGGGGCAGCAGCCGCCGCCGCAGG
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Pred. No. 0.
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa US-09-252-991A-14293
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Best Local Similarity 48.1%;
Matches 150; Conservative
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US-09-252-991A-14293
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US-09-252-991A-6276
US-09-252-991A-6276

y Bequence 6276, Application US/09252991A

patent No. 6551795

y GENERAL INFORMATION:
    APPLICANT
    MITCH OF INVENTION:
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
    TITLE OF INVENTION: NUMBER: US/09/252,991A
    CURRENT APPLICATION NUMBER: US 60/074,788
    PRIOR APPLICATION NUMBER: US 60/074,788
    PRIOR PILING DATE: 1998-02-18
    PRIOR PILING DATE: 1998-02-18
    PRIOR PILING DATE: 1998-07-27
    NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 6276
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                                                                                                                                            883 CGCTGGTGGTCGCCGGCCTGCTGCCCGGCGCCGGCTTGCTCAGCGACCGCCTTGGCCACA
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Pred. No. 0.11;
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0; Mismatches 162; Indels
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6276
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Best Local Similarity 45.9%;
Matches 180; Conservative
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Matches 150; Conservative
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Sequence 193, App
Sequence 193, App
Sequence 8, Appli
Sequence 1, Appli
Sequence 1483, Ap
Sequence 193, App
                                                                                                             November 29, 2003, 15:12:39 ; Search time 353 Seconds (without alignments) 8866.730 Million cell updates/sec
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'(cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
'(cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
'(cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Compugen Ltd
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US-10-023-529-45

US-010-023-523-45

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US-10-023-523-50

US-10-203-523-50

US-10-203-523-50

US-10-203-523-50

US-10-203-523-50

US-10-203-523-50

US-09-827-688-8

US-09-827-688-8

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US-10-116-275-197
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US-09-814-353-19995
US-10-037-270-713
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Maximum Match 100%
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  Sequence 1481,
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Sequence 41,
Sequence 46,
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US-10-156-761-15103

US-10-156-761-15103

US-10-156-761-15103

US-10-287-218-41

US-10-287-218-41

US-10-287-218-41

US-10-329-079-46

US-10-329-079-46

US-10-023-529-48

US-10-023-529-48

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US-10-029-079-14

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JERNERAL INFORMATION:

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: NOWER: 2001-12-17

CURRENT APPLICATION NUMBER: US/09/616,289

PRIOR PPLING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR PILING DATE: 1900-03-02

PRIOR PPLING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR PLING DATE: 1997-11-27

PRIOR PLING DATE: 1996-11-27

PRIOR PLING DATE: 1997-11-26

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6.8%; Score 64.6; DB 13;
Best Local Similarity 46.4%; Pred. No. 7.2e-06;
Matches 211; Conservative 0; Mismatches 244;
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; LOCATION: (1)...(1614)
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APPLICANT: Law, Simon W.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/516,289
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.2e-06;
0; Mismatches 244; Indels
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GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicAN
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APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Aribal A.
TITLE OF INVENTION: Anibal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
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Pred. No. 1.3e-05;
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PRIOR APPLICATION NUMBER: 09/616,289
PRIOR APPLICATION NUMBER: 08 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-03
PRIOR FILING DATE: 1996-03
PRIOR FILING DATE: 1996-03
NUMBER: OF SEQ ID NOS: 53
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 50
LENGTH: 12425
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Publication No. US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATTEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-1-10-12
PRIOR APPLICATION NUMBER: US 08/919,608
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PELING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FREUESQ FOR WINGOWS VERSION 4.0
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Pred. No. 1.3e-05;
0; Mismatches 244; Indels 0;
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APPLICANT: Lees, Ann M. APPLICANT: Lees, Robert S. APPLICANT: Lees, Robert S.
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; ORGANISM: Homo sapiens
US-09-976-740-50
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US-09-976-740-50/c
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US-10-200-562-193/C
is Sequence 193, Application US/10200562
; Sequence 193, Application US/10200562
; Publication No. US20030165819A1
; GENERAL INFORMATION:
; APPLICANT: McGowen, Patrick
; APPLICANT: Hosken, Nancy A.;
; TITLE OF INVENTION: TRRATMENT OF HERPES SIMPLEX VIRUS INFECTION
; TITLE OF INVENTION: TRRATMENT OF HERPES SIMPLEX VIRUS INFECTION
; TITLE OF INVENTION: 1282C2
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 3957
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45.8%; Pred. No. 1.8e-05;
tive 0; Mismatches 301;
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ORGANISM: HSV2
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ANGRER: US/10/023,523
CURRENT APPLICATION NUMBER: US/20/616,289
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 1997-11-26
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Pred. No. 1.3e-05;
0; Mismatches 244; Indels 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020152485A1
GENERAL INFORMATION:
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Publication No. US20030165820A1
GENERAL INFORMATION:
APPLICANT: Day, Craig H.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TATATHEN OF HERPES SIMPLEX VIRUS INFECTION
TITLE OF INVENTION: TATATHEN UNBER: US/10/237,551
CURRENT APPLICATION NUMBER: US/10/237,551
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 2202
SOFTWARE: FREESEQ for Windows Version 4.0
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Sequence 8, Application US/09827688
Publication No. US20030165476A1
GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION DI
TITLE OF INVENTION: AGENTS
FILE REPERENCE: PO1949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT PILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-07
ONTHER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63.4; DB 12;
Pred. No. 5.4e-05;
                                                                                                                    2052 cesescesceseseseseseseseseses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 GATGATGTGCCGGCTGTCGGAGCCC
668 GATGATGTGCCGGCTGTCGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 8
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APPLICANT: Farnet, Chris
APPLICANT: Zazogoulos, Emmanuel
APPLICANT: Staffe, Affredo
APPLICANT: Staffe, Affredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILLING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (13617)...(12802)
OTHER INFORMATION: ORF 9; negative strandedness
NAME/KEY: misc_feature
LOCATION: (15203)...(13614)
OTHER INFORMATION: ORF 10; negative strandedness
NAME/KEY: misc_feature
LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11; positive strandedness
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (15880)...(19035)
OTHER INFORMATION: ORF 12; positive strandedness
NAME/KEY: misc_feature
LOCATION: (19032)...(39713)
OTHER INFORMATION: ORF 13; positive strandedness
NAME/KEY: misc_feature
LOCATION: (39713)...(65800)
OTHER INFORMATION: ORF 14; positive strandedness
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17, positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 positive strandedness
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (2077)..(3078)
OTHER INFORMATION: ORF 1; positive strandedness
NAME/KEY: misc feature
LOCATION: (3118)..(4032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (7703) .. (6693)
OTHER INFORMATION: ORF 5; negative strandedness
NAME/KEY: misc_feature
LOCATION: (9464) .. (8130)
OTHER INFORMATION: ORF 6; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (9691)..(10761)
OTHER INFORMATION: ORP 7; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (403\overline{6})..(5048)
OTHER INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2; positive strandedness
                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
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OTHER INFORMATION: ORF 16;
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15;
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Actinoplanes sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (4038)..(504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (13617)..(12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 88421
                                                                                                                                          APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
ITILE OF INVENTION: AGENTS
FILE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152296 GACGACGCCAGCCCCCTGCGGGTCGGGGCCCTCGGCGGGCCGGCGGGTCAGCGCCGCGG 152237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151996 TCTGGAAGAGCAGGTCCGCGGCGGCGCGGCGGGGGCTCAGCAGCCGCGGGTCCGCG 151937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151876 cercidentecedecedecedecededagir----cecedecedagedarcagededecensistas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152056 GCGCGGCGACCGACTCGCCCGCGCGCGTGTCGGCCAGCAGGGGGCGCACACTCTGGT 151997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 GGTCGAGCGGCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGGCCCGCT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 GAGCCGCGAGTGCCGCTGCCGCCATCCGGAGCATGGTCAGGGGCTACGAGGAGGCCAT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 GGCGGCGGCGCCGCTGTGCTTCGCGGCCCTGGTGGCCGTGGCCGTCTGCCAAGGCGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 GCCGCCGCTGGAGAAAGGCTGGTGGCCATGGGGCCGCCGCAGCAGCCGCCGCCGCCGCAGGG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 CTACGGTCAGGGTGGCCAGCGGCAGATGTATCCACCGTGTCGTCCCGGCACCACCGGCGG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 CGGGCCAAGGATCGGCCGCGTGAGGCTTACGAAGGCCCGGGAGTACGCCGCGGGGTTGCC 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 CGACGCGTGCCGCCAGGTCCTCGACCGGCAGCTAACCGGCGGCGGCGGCGGCGGCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 TGGCCCGTTCCGGTGGGGCACCGGGCTCCGGATGCGGTGCTGCCAGCAGCTCCAGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 154746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63.4; DB 12; Length
Pred. No. 5.4e-05;
0; Mismatches 301; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151761 cecececececececececece
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                                                        Sequence 8, Application US/09827688 Publication No. US20030165476A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-976-059-1
; Sequence 1, Application US/09976059
; Patent No. US20020164747A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 154746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.8
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HERPESVIRUS 2
US-09-827-688-8
                                      JS-09-827-688-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ઠે 움 셤 ઠે LOCATION: (70099)..(70662) OTHER INFORMATION: ORF 18; positive strandedness NAME/KEY: misc\_feature

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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: ARBURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PAECHLIN Ver: 2.1
SEQ ID NO 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMEN'EXE: modified base LOCATION: (124)..(129)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified base
LOCATION: (146)..([148)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base
LOCATION: (151)..(Ī52)
JTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATION: (155) -
THER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g, unknown or other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g, unknown or other
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          Sequence 1483, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified base
LOCATION: (185)..(188)
OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCATION: (192)
THER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified base LOCATION: (1)...(118)
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LOCATION: (172)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base
LOCATION: (179)..(T80)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
COCATION: (182)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
(201)..(2933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(3133)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
LOCATION: source
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67861 TGGCCGGCGGCGTCGCCAAGGTCCTCGCCCGGTACGAGCCGGGCGCGGCTGCGGGCTCG 67920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67741 GCGGAACCGCGACGCGCCGCCTCGGCCGCGCCCTGGGGCCTGGGCCTGGGCGACGGCGGC 67800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 CCGCTCGACGCGTGCCGCCAGGTCCTCGACCGGCAGCTAACCG--GCGGCGGCGGCGGCGGCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GCGGCGTTGGCCCGTTCCGGTGGGGCACCGGGCTCCGGATGCGGTGCTGCCAGCAGCTCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 GGCGAGGTCGAGCGCGCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGGCCAGGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.6%; Score 63; DB 10; Length 88421; Best Local Similarity 54.6%; Pred. No. 5.8e-05; Matches 147; Conservative 0; Mismatches 120; Indels 2
                                                                                                                                                                                                                                                                                                                   DCCATION: (75535). (76464)
OTHER INFORMATION: ORF 23; positive strandedness
LOCATION: (7810). (7649)
OTHER INFORMATION: ORF 24; negative strandedness
NAME/KEY: misc feature
LOCATION: (7884). (7649)
OTHER INFORMATION: ORF 24; negative strandedness
NAME/KEY: misc feature
LOCATION: (79864). (7810)
OTHER INFORMATION: ORF 25; negative strandedness
NAME/KEY: misc feature
LOCATION: (81624). (79861)
OTHER INFORMATION: ORF 26; negative strandedness
LOCATION: (70659)..(71906)
OTHER INFORMATION: OR 19; positive strandedness
NAME/KEY: misc_feature
LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (85556)...(86845)
OTHER INFORMATION: ORF 31; positive strandedness NAME/KEY: misc_feature
LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32; positive strandedness
                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21; negative strandedness
                                                                                                                                                                                                                    KEY: misc_feature
TION: (75424)..(74213)
INFORMATION: ORF 22; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEY: misc_feature
ION: (81909)..(81682)
INFORMATION: ORF 27, negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /KEY: misc_feature
:ION: (82346)..(82062)

INFORMATION: ORF 28; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (82587)..(84446)
INFORMATION: ORF 29; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /KEY: misc_feature
|TON: (84481)..(85548)
| INFORMATION: ORF 30; positive strandedness
/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67981 GCCTCGGGCTCCGGCGCCGCCGCGGTCCC 68009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AGGACGTGAGCCGCGAGTGCCGCTGCGCC 389
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
COCATION: (75535)..(764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-017-161-1483
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unknown	unknown	1. 1. 1.	TIN COMMITTEE OF THE CO	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown	unknown
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ϋ	ບັ		ວັ	ΰ	ú	ú	ບໍ	υ ,	ΰ	ú	· J	ີ່	υ ,	ú	υ ,	ΰ	ΰ	ΰ	່ວ
OTHER INFORMATION: a, t, FRATIRE:	NAME/KEY: modified_base LOCATION: (210) OTHER INFORMATION: a, t,	раве	a, c,	a, t,	NAME/KEY: modified_base LOCATION: (219) OTHER INFORMATION: a, t,	base 225) a, t,	: modified_base : (229) FORMATION: a, t,	ge (t	ْئ يو	FEATURE: NAME: modified_base LOCATION: (242) OTHER INFORMATION: a, t,	base a, t,	base 260) a, t,	FEATURE: NAME/KEY: modified base LOCATION: (265)(270) OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: modified base LOCATION: $(272) (\overline{2}76)$ OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: modified_base LOCATION: (278) OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: modified base LOCATION: (282)(283) OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: LOCATION: (287)(290) OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: LOCATION: (302)(306) OTHER INFORMATION: a, t,	FEATURE: NAME/KEY: modified base LOCATION: (311)(313) OTHER INFORMATION: a, t,

129 geogeogeogeogeogerargerrogogeocorrogrageograficarogeogae 188 249 GACGCGTGCCGCCAGGTCCTCGACCGGCAGCTAACCGGCGGCGGCGGCGGCGGCGGCGTT 308 GGCCCGTTCCGGTGGGGCACCGGGTCCGGATGCGGTGCTCCCAGCAGCTCCAGGACGTG 368 189 GTCGAGCGGCAGAGGCTCAGGGACCTGCAGTGCTGGCAGGAGGTCCAGGAGAGCCCGCTC 248 454 chocacionannecaciocacachecanacacannacacannacanacanacachecaca 513 0; Gaps Query Match 6.4%; Score 61.2; DB 12; Length 3133; Best Local Similarity 34.6%; Pred. No. 5.9e-05; Matches 198; Conservative 0; Mismatches 374; Indels 0; NAME/KEY: modified base
LOCATION: (323)...(334)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (336)...(341)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (345)...(363)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (365)...(368)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (370)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(385)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(385)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(388)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(389)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(389)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (379)...(389)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (379)...(389)
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NAME/KEY: modified base
LOCATION: (379)...(389)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (379)...(389)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (379)...(389) FEATURE:
NAME/KEY: modified\_base
LOCATION: (409)
OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (400)...(402) OTHER INFORMATION: a, t, c, g, unknown or other c, g, unknown or other c, g, unknown or other NAME/KEY: modified\_base LOCATION: (395) OTHER INFORMATION: a, t, c, FEATURE: NAME/KEY: modified\_base LOCATION: (397) OTHER INFORMATION: a, t, c, FEATURE: NAME/KEY: modified\_base 309 g ò g 8 셤 ઠે ð

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290 CGGCGGCGCCGCGGCGCTTGCCCGTTCCCGTGGGGCACCGGGCTCCGGATGCGGTGCTG 349
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833 TGTCGCACCCCGCGGCGGCCGCCCATGAACATGCCGTCCGGGCTGCCGC--ACCCCGG 890
                                                                                                                               350 CCAGCAGCTCCAGGACGTGAGCCGCGAGTGCCGCTGCGCCGCCATCCGGAGCATGGTCAG 409
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                                                                    445 GCTGGTGGCCATGGGGGCGGCAGCAGCCGCCGCCGCAGGGAGGAGGAGAGAGAG
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.2%; Score 59; DB 10; Length 30 Best Local Similarity 52.2%; Pred. No. 0.0002; Matches 131; Conservative '0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 311
LENGTH: 3035
                                                                                                                                                                                                                                                                  951 GCAGGTGGCAGCGCATCGGCGGCGCGC 977
                                                                                                                                                                                                    505 GGGCTACTACTACCCCTGCAGCCGGC
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Publication No. US20030165831A1
GENERAL INFORMATION:
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Dillon, Davin C.
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Lodes, Michael J.
Algate, Paul A.
Fling, Steve P.
Mannion, Jane
Benson, Darin R.
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APPLICANT: Thompson, Pame
APPLICANT: Lillie, James
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   773 GCGGCGGGCTCCTGGGCGGCTCCGCGCACCCTCACCCGCATATGCACAGCCTGGGCCACAC
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48.8%; Pred. No. 0.00017;
iive 0; Mismatches 196; Indels 2;
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Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: BIAN PHARMACHLICAL
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
ITILE OF INVENTION: Genetic Analysis of Peyen
ITILE OF INVENTION: Compositions Targeting if FILE REFERENCE: B1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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US-10-116-275-197
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Best Local Similarity
Matches 189; Conserv
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INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 12; Length 339
Pred. No. 0.00021;
0; Mismatches 120; Indels
                                                                TITLE OF INVENTION: THERAPY OF OVARIAN CANCIS
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-55
PRIOR APPLICATION NUMBER: US 60/201,940
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASSES OF WINDOWS VERSION 4.0
SSOFTWARE: PASSES OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.2%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353-19995
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Search completed: November 29, 2003, 17:04:01 Job time : 371 secs

Human protein Friz

AAU74823 AAE34057 ABU55903 ABB59015 ABB62974 ABB57126

Drosophila melanog

Drosophila melanog Drosophila melanog Mouse ischaemic co A HOOROS9 polypept Human polypeptide Human polypeptide Human NFAR-2 SEQ I Human Dolypeptide Human EWS protein Human EWS protein Human EWS protein Human EWS protein Drosophila melanog Human polypeptide Amylase inhibitor Wheat amylase inhibitor Wheat amylase inhibitor in Novel maylase inhibitor

AAW97318 AAM39887 AAM41673 AAB35806 AAB35148 ABP63025 ABP63025

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AAR44555 AAW33813 ABG06460 ABB65135 AAC05578 AAR58636 AAR29525 AAW24493 AAB28185 ABP63092

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Amino acid sequenc Polypeptide encode Human DITHP intrac Novel human diagno

Peanut allergen Ar Part of the sequen Amino acid sequenc Drosophila melanog

AAY84357 AAR47481 ABR41261 AAB82383 AAP91891 AAY84354 ABB61917

**ALIGNMENTS** 

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WPI; 2002-017612/02.
N-PSDB; AAI70852.
  Triticum aestivum.
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Rice seed allergen
Flax 2S storage pr
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| SIDSI/gcgdata/geneseq_geneseqp_embl/AA1980.DAT:*
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                                                                                                                                                                                                                                                                       1 MAKIAAAAAALCFAALVAV........MMCRLSEPQECSIFSGGDQY
                     GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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AAW53261
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AAR31036
ABJ26643
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Gapop 10.0 , Gapext 0.5
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new nucleic acid comprising a variant allele of the 1Ax2asteriskHMW Wheat; glutenin; storage protein; variant; transgenic plant; gluten. Lang ۲, Karsai Ö Wheat glutenin variant 1Ax2asteriskB Vida Ş AAM50386 standard; Protein; 434 Juhasz A, Tamas L, Bedo Z, Tamasne Nyitrai E; 13-APR-2001; 2001WO-HU00045. 14-APR-2000; 2000HU-0001563 entry) (MAGY ) MTA MEZOGAZDASAGI 

> Result 8

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WPI; 1998-179218/16.
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glutenin subunit gene of wheat has at least one extra cysteine codon and is useful for developing new wheat varieties with enhanced quality gluten -
                                                                                                                                                                                                                                                                           11 ALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGVGPFR
                                                                                                                                                                                                                                                                                                                                    71 WGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWP-------
                                                                                  designated laxiasterisks, of laxiasterisk HWW glutenin, found in certain lines of wheat variety Bankuti 1201. The variant gene (see AAI70852) differs from the laxiasterisk gene by a single point mutation of C to G. This results in a change from Ser to Cys at amino acid position 394 of the encoded protein. Because of this, the newly identified allele provides enhanced possibilities for the formation of disulfide bridges compared with the known allele, which could at least partly the newly identified gene can be used to develop transgenic wheat varieties with better quality gluten.
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viscoelastic property; wheat flour; wheat dough; bread; noodle.
                                                                                                                                                                                                                                                     43; Indels 128;
                                                                                                                                                                                                                                Length 434;
                                                                          The present sequence is that of the newly identified allele,
                                                                                                                                                                                                                                                                                               AAVVVALVALTAAEGEASGO----LOCERELOEHSLKACROVVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of Synthetic HMW-glutenin protein.
                                                                                                                                                                                                                                ; Score 156; DB 23;
; Pred. No. 2.5e-06;
17; Mismatches 43;
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                                                     Disclosure; Fig 6; 28pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 QQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWPWGRQQQPPPQ-----GGGGGGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GYYYP---CSRPGEGYGYGYGQGQRQMYP----PCRPGTT---GGGPRIGRVRLTKAREYA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 KRYYPSVTCPQ------QVSYYPGQASPQRSSSSYHVSVEHQAASLKVAKAQQLA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 QGEVERQRLRDLQC---WQEVQESPLDACRQVLDRQLTGGGGGGGGGGFRWGTGLRMRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 QOLRDISPECHPVVVSPVAGQYEQQIVVPP--KGGTFYPGETTPPQQLQQRIFWGIPALL
                                                                                                                                                                                           This amino acid sequence is of the synthetic HWW-glutenin protein which is introduced into the DNA of the cereal to form a non-natural repetitive domain which changes the viscoelastic property of a dough. The domain comprises HWW glutenin subunit repeats which are synthetic in sequence or non-natural in number. The dough is useful for making a wheat flour, wheat dough, bread or noodle.
A process for altering the visco:elasticity of a dough - comprises genetic engineering of a high molecular weight glutenin subunit containing a non-natural repetitive domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 15438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EGEASEQ----LQCDRELQERELKACQQVMD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.4%; Score 130.5; DB 27.2%; Pred. No. 0.0002; tive 21; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AGLPMMCRLSEPQECSIFSGGD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                        Example 2; Page 18; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB62882 standard; Protein; 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
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Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AQLPAMCRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL06985
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                                                                                                                                                                                                   103 EEAMPPLEKGW---WPW---GRQQQP------PPQGGGGGGGGGYYYPCSRPG-EGY 145
                                                                                                                                                                                                                       107 QOPTPP---GWPPGWQWGAGGNQNQPGFDWVQTGFAPGWNGGGGQG------PGWNGP 155
                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Improving yield of natural conformation of disulphide bridge proteins - obtd. by transformed prokaryotic host cells, by adding thiol reagent, esp. glutathione, to culture medium
                                                                                                                                                                                 30;
Disclosure; SEQ ID NO 15438; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of alpha-amylase/trypsin inhibitor (RBI) from Eleusine coracana with an OmpA signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                        Protein disulphide isomerase; RBI; disulphide bridge protein.
                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                                                                                                                                                                    Alpha-amylase/trypsin inhibitor with OmpA signal peptide.
                                                                                                                                                                                17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rudolph
                                                                                                                                                           Score 117; DB 22;
Pred. No. 0.0094;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "OmpA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "RBI mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wunderlich M, Skerra A,
                                                                                                                                                                                                                                                             GWNGGGGRG--PPPRPGFNGGGP 176
                                                                                                                                                                                                                                            GYGQGGQRQMYPPCRPGTTGGGP 168
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                                                                                                                                                                                                                                                                                                                AAR28122 standard; Protein; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 10; 18pp; German.
                                                                                                                                                            10.2%;
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                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                33; Conservative
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                                                                                                                                                                     Local Similarity
                                                                                                                                         362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ29910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glockshuber R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1992;
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17-MAR-1993
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                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                            146
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                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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AAR28122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWPWGRQQ 120
                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                     1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG
                                                                                                                                                                                                                                                                                                                                                                           1 MKKTAIAIAVALAGFATVA----QASVGTSCIPGM----AIPHNPLDSCRWYVSTRTC--
                                                                                                                                                                                                                                     47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ÓDLP------GCPRQVÓRAFAPKLVTEVECNLAÍIHGGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QPPPQGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYP-----PCRPGTTGGGP
                                                                                                                                                                  ch 10.0%; Score 114.5; DB 13; Length 143; 1 Similarity 26.4%; Pred. No. 0.0058; 46; Conservative 17; Mismatches 64; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 42156; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 42156
See also AAR28123 and AAR28124. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB71788 standard; Protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
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                                                                                                      143 AA;
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                                                                                                      Sequence
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Best Local
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| | | : | : | : | : | : | : | 658 WAEYYRSVGKIEEAEAIEKTLKNKQQNGSGGQSSTPNPSQGGSGG-----QQPNPAAAAA 712
                                                                                                713 AAAAAAAAGGYGQSMTPTQYAQYSQYYAAAAAAGGQPQGAPQPGGGQSGGPPGNYPGNY 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of Comamonas acidovorans A:18 stereospecific hydrolase which can be used in the prodn. of optically pure S-(+)-2,2-dimethylcyclo propane carboxamide (2,2-DMCPCA)., the starting material for the prodn. of cilastatin. Cilastatin inhibits e.g. renal dehydropeptidase (RDP) and in therapy it is administered with the antibitic penem or carbapenem to prevent their inactivation by RDP. (Updated on 25-MAR-2003 to correct PN field.)
                                                             91 RCAAIRSMVRGYEEAMPPLEKGWWPW-----GRQQQPPPQGGGGGGGG-YYYPCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-terminal peptide used to obtain AAQ35116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pure S-(+)-2,2-di:methyl:cyclopropane carboxamide prodn. by microorganisms(s) - with a stereospecific hydrolase isolated from microorganism, useful for inhibition of renal dehydro:peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-(+)-2,2-dimethylcyclopropane carboxamide; 2,2-DMCPCA; prodn.;
cilastatin; antibiotic therapy; penem; carbapenem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "peptide used to obtain AAQ35117"
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llarity 22.8%; Pred. No. 0.057;
Conservative 16; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birch OM, Boehlen E;
                                                                                                                                                                                                                                                                                                                                                                                                                       C. acidovorans stereospecific hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                AAR31036 standard; Protein; 426 AA.
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                                                                                                                                           141 PGEGYG--YGQGGQRQ 154
                                                                                                                                                                               773 PGAGYGGYPGAPGOOO 788
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                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
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N-PSDB; AAQ38949.
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26-MAY-1993
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                                                                                                                                                                                                                                                                                                                        AAR31036;
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Best Local (
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL161064 ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                             91 RCAAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGGG 150
                                                                                                                                                                                                  ---GDRGQGGG------GWGGQNRQNGGGNWGGAGGGGFGNSGGNFGGQGGGSG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                 35 LOCWQEVQESPLDA----CRQVLDRQLTGGGGGGGGGGFRWGTGLRMRCCQQLQDVSREC
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                             40;
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  Score 110; DB 22; Length 385;
Pred. No. 0.046;
7; Mismatches 50; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 797;
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9.6%; Score 110; DB 22; Length 79
Best Local Similarity 30.1%; Pred. No. 0.1;
Matches 41; Conservative 14; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 19008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                              ABB64072 standard; Protein; 797 AA.
                                                                                                                                                                                                                                           151 GQRQMYPPCRPGTTGGGP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWD,
                                                                                                                                                                                                                                                                                264 GWNQQ-----GGSGGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001, 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                          41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-656860/75.
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                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABL08175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
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    Query Match
Best Local S
Matches 41
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                                                                                                                                                                                                    217
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12;
                                               99
DB 14; Length 426;
                        IndelB
                                               24 QGEVERQRLRDLQCWQEVQESPLD--ACRQVLDRQLTGGGGGGGV-
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38 WQEVQES----PLDACRQVL-DRQLTGGGGGGGV-GPFRWGTGLRMRCCQQLQDVSREC 90

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                                                                                                                                                                                                                ------GWWP---WGRQQQPPPQGGGGGGGG 133
                                                                                                                                                                                                                                                                                  227 ARGHRRGGPAGPYGQPVQRARLSGHDDARILRPAPGHGPAMGTGRRGCPLPPGGGAGPGG 286
                                                                                                                                                                                                                                                                                                                                                                                                                          -----GAAPGGQRAGGPLSRCHPG--GGGLAGAVRGGDRRGARRHVPCTARGL 332
123 QAAADRRRIRRPPSRDHCPRQPLERPAMARGLVQRLGRGHGGGAVLRIAGHRGLHPLS 182
                                                                                                                                           183 IGRQRHHGAQAHLGQGEPPRRLRTGRVPGPHR--------PDGAOCCRC---RSH
                                                                         -GPFRWGTGLRMRCCQQLQDVSRECRCAAIRSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide applicable in examination Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 109; DB 24; Length 166;
86.0%; Pred. No. 0.022;
ve 11; Mismatches 44; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 -PRIGRVRLTKAREYAAGLPMMCR----LSEPQECSIFSGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 WPRARRVDRPGAGPVRHRLPAAAAAPRGLHGPGACTLRAGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice; Chrohn's disease antibody-binding peptide;
human vacuolar H+ transport ATPase; rice allergen
human kruppel-like zinc finger protein 300.
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                                                                                                                                                                                                                                                                                                                                                    134 YYYPCSRPGEGYGYGQGGQRQMYP--PCRPGTTGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice seed allergen protein - SEQ ID No 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ26643 standard; Protein; 166 AA
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                                                                                                                                                                                                             VRGYEEAMP-----PLEK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-2001; 2001JP-0126121.
25-FEB-2002; 2002JP-0047384.
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The present sequence is a flax 2S storage protein.

The present invention relates to a method for expressing non-native genes in flax seeds. The method comprises introducing a chimeric nucleic acid construct containing a seed-specific promoter obtained from flax and a nucleic acid which is non-native to the promoter, into a flax plant cell and growing the plant cell into a mature flax plant capable of setting seed, where the nucleic acid is expressed in the seed under the control of the promoter. The seed-specific promoters obtained from flax are useful for modifying the protein, oil or polysaccharide composition of the flax seeds and seeds of other plant species. The promoters facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of proteins, including sulphur-rich protein that are found in uppins or Brazil nutes in a seed deficient in sulphurous amino acids, peptides having pharmaceutical value such as anticoagulants, antibodies, vaccines, cytokines, growth factors, interleukins, mammalian proteins, including alpha-1-antitrypsin, anti-obesity proteins, haemoglobin, blood proteins, human serum albumin, insulin, lactoferrin, myoglobin, pulmonary surfactants and proteins of industrial value such as alpha-amylase, arabinase, amyloglucosidase, catalase, cellobiohydrolase, pectinases,
--PMAEVFPGCRRGD- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressing non-native genes in flax seeds and seeds of other plant species for altering the seed oil and protein composition in the seeds, comprises using seed-specific promoters obtained from flax -
                                                                                                                                                                                                                                                                                                                                                   Flax; seed-specific promoter; storage protein; seed oil; vaccine; protein expression; anticoagulant; cytokine; growth factor; pectinase; interleukin; alpha-1-antitrypsin; anti-obesity protein; haemoglobin; serum albumin; insulin; lactoferrin; myoglobin; pulmonary surfactant;
                    ----GGIYRELGATDVGH--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Glutamine-rich region"
                                                                                              -------LERA---AASLPAFCNVDIP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moloney MM,
                                                          165 GGGPRIGRVRLTKAREYAAGLPMMCRLSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                               Ŕ
                                                                                                                                                                                           AAY72901 standard; Protein; 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Fig 3; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEMB-) SEMBIOSYS GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaudhary S, Van Rooijen G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phytase, papain and xylanase.
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                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                              Flax 2S storage protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha amylase.
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                    103
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52 LPRCRAVVKROCVGHGAPGGAVDEQ----LRODCCROLAAVDDSWCRCSALNHWV---- 102

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46 LDACRQVLDRQLTGGGGGGGGGGGGGTGLRMRCCQQLQDVSRE-CRCAAIRSMVRGYEE

Best Local Similarity 26.0 Matches 39; Conservative

105 AMPPLEKGWWPWGRQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPGTT 164

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6; Fig 24; 135pp; English
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       Claim
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                                                                                                                                    58 TGGGGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWPWG 117
                                                                                                                         RQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGGGGQRQMY-----PPCRPGTTGGGP 168
                                                        57
                                                                       34
                                                                                                                                                                     ---RIGRVR-----LIKAREYAAGLPMMCRLSEPQECSIFSGGDQ 205
                                                                                                                                                                                                                                                                                     Fruit fly; gene expression; dicer; argonaute 2; RNA interference; RNAi; attenuation; gene function.
                                                        1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQ----VLDRQL
                                                                        ------DASVRITVIIDEET
                                                                                                          35 NQGRGGGKV----AGTAAVCEQQIQQ-----RDFLRSCQQFM-----WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attenuating gene expression in a cell using gene-targeted double stranded RNA -
                      9.3%; Score 106.5; DB 22; Length 174; 22.6%; Pred. No. 0.04; ive 25; Mismatches . 57; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                        1112..1119
/note= "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                                               /note= "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                               "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                       437..446
/note= "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                               "Peptide identified by microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hammond S,
                                                                                                                                                                                                                                                                      Drosophila melanogaster argonaute 2 protein.
                                                                        1 MAKLMSLAAVATQFLFLIVV------
                                                                                                                                                                                                                    AAE09770 standard; Protein; 1145 AA
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caudy A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICA INC.
COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001WO-US08435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0189739.
2000US-0243097.
                                                                                                                                                                                                                                                     (first entry)
                              Local Similarity 22.6 es 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                       .488
                                                                                                                                                                                                                                                                                                                                                                                        548..558
                                                                                                                                                                                                                                                                                                                                                                                                       593..605
                                                                                                                                                                                                                                                                                                                                                                                                                         740..746
                                                                                                                                                                                                                                                                                                                                                        456..462
                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-565793/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200168836-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000;
24-OCT-2000;
                                                                                                                                                                                                                                                     29-NOV-2001
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                                                                                                                                                           169
                                                                                                                         118
                                                                                                                                                                                                                                    AAE09770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beach D,
       Sequence
                      Query Match
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                                                                                                                                                                                                                                                                                                                                       Region
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                                       Matches
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The invention relates to methods for attenuating gene expression in a cell using gene targetted double stranded RNA. The double stranded RNA comprises a nucleotide sequence that hybridises under physiologic conditions of the cell to the DNA sequence of the target gene to be inhibited. The method utilises a cell in which dicer or argonaute activities are recombinantly expressed or otherwise ectopically activities are recombinantly expressed or otherwise ectopically activated. Activated RNA interference (RNAi) enzymes such as dicer and argonaute are specifically and potently used for inactivating a cloned gene and proves to be a powerful tool for investigating gene function. Methods are used for attenuating target gene expression in non-embryonic cells suspended in culture or in animals. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 QQLQQPQ--QQQQQQPHQQQQQSSRQQPSTSSGGSRASGFQQGGQQQKSQDAEGWTAQKK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 RCCQQLQDVSRECRCA----AIRSMVRGYEEAMPPLEKGWWPWGRQ------QQPPP--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEPTR; human; antiinflammatory; cytostatic; immunosuppressive;

antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic;

meuroprotective; antiallargic; antibody; immunogen; endometriosis;

meuroprotective; antiallargic; antibody; immunogen; endometriosis;

metrointestinal disorder; gastritis; oesophageal carcinoma;

crohn's disease; irritable bowel syndrome; ulcerative colitis;

endocrine disease; inflammatory disease; infertility; receptor;

autoimmune disease; inflammatory disease; infertility; receptor;

acquired immune deficiency syndrome; AIDS; rheumatoid arthritis;

allergy; osteoarthritis; diabetes mellitus; multiple sclerosis;

systemic lupus erythematosus; cell prodiferative disorder;

specemic lupus erythematosus; cell prodiferative disorder;

mecker muscular dystrophy; neurological disorder; epilepsy;

Alzheimer's disease; Huntington's disease; reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster argonaute 2 protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 ----QGGGGGGGYYY-PCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 QGGHQQGRQGQEGGYQQRPSGQQQGGQGGHQQGRQGQEGGYQQRPPGQQGGGHQQGR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.3%; Score 106.5; DB 22; Length
Best Local Similarity 25.9%; Pred. No. 0.33;
Matches 45; Conservative 25; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 QRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGFRWG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-2000; 2000US-214027P.
25-AUG-2000; 2000US-228045P.
12-DEC-2000; 2000US-255104P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1145 AA;
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This invention relates to twelve human receptors CDNA sequences
referred to as REPTR-1 to REPTR-12), and the proteins encoded thereby.
The proteins of the invention may have antifinflammatory, cytostatic,
immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
general, anticonvulsant, noctropic, neuroprotective, antiallergic
activities. The sequences of the invention may be used to produce REPTR
agonists or antagonists, and the protein sequences may be used to raise
anti-REPTR antibodies. These molecules and the REPTR polymucleotides and
polypeptides of the invention are useful in the diagnosis, treatment and
prevention of gastroincestinal (e.g. gastritis, oesophageal carcinoma,
crohn's disease, irritable bowel syndrome, ulcerative colitis),
endocrine (e.g. hypothalamus disorder, Kallman's disease), autoimmune/
inflammatory (e.g. acquired immune deficiency syndrome (AIDS),
renumatoid arthritis, allergies, osteoarthritis, diabetes mallitus,
multiple sclerosis, systemic lupus erythematosus), cell proliferative
(e.g. cancer), developmental (e.g. Duchenne and Becker muscular
disorders. Numerous other examples of each disorder are given in the
specification. The present sequence represents the human REPTR6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 KFFLCSMYTPICLEDYKKPLPPCRSVCER-----AKAGCAPLMRQYGFAWPD--RMRCD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 QQLQDVSRECRC----AAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 RLPEQGNPDTLCMDYNRTDLTTAAPSPPRRLPPPPPG------EQPPSGSGHGRP--- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 Q------FRWGTGLRACRQVLDRQLTGGGGGGGGGGGGGGGGGGGGGRARCC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- EVER-ORLRDLQCWQEV 41
  Tang YT;
Burford N;
                                                                                                                                                                  Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell proliferative (e.g. cancer)disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                           Xu Y;
Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
  Nguyen DB,
R, Yao MG,
C, Yang J,
Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drug screening; toxicology assay; signalling pathway; FZD 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1%; Score 105; DB 23; Length 6 23.7%; Pred. No. 0.26; tive 22; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
Griffin JA, Kallick DA, Tribouley CM, Yue H,
Lal P, Policky JL, Azimzai Y, Lu DAM, Graul
Hafalia AJA, Baughn MR, Bandman O, Patterson
Gandhi AR, Warren BA, Ding L, Sanjanwala MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - PGARPPHRGGGRGGGGDAAAPPARGGGGGKAR 219
                                                                                                                                                                                                                                                                      Claim 50; Page 119-121; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AAAAAALCFAALVAVAVCQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE34057 standard; Protein; 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of the invention
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Matches 51, Conservative
                                                                                                        2002-090432/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 AA;
                                                                                                        WPI; 2002-090432/
N-PSDB; ABK15174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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IID AAE3
XX
AC AAE3
XX
DT 02-P
DT XX
DE FZD
XX
KW Drug
OS Unic
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The present invention relates to a novel screening method which enables the identification of biologically active agents which mediate their effect through the activation of genes. The method involves providing a population of cells stably transfected with a nucleic acid encoding a reporter molecule, cloning the transfected with a nucleic acid encoding a reporter molecule, cloning the transfected cells into a cell array, signal generated by the reporter molecule as a result of exposure to the agent. The method is useful in identifying biologically active agents and the genes through which the agents act, in screening potential drugs of the their ability to activate certain drug targets in a high-throughput assay, in identifying relationships between signalling pathways and specific signals that could be useful in eventually directing the differentiation of embryonic stem cells and in toxicology assays by testing for unwanted activation or inhibition of specific signalling pathways. The present sequence is FZD 8 protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 QQLQDVSRECRC----AAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EVER-ORLRDLOCWOEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AAAASAKELACQEITVPLCKGIGYNYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 Q------PRWGTGLBACKQVLDRQLTGGGGGGGGVGP-----PRWGTGLRMRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 KFFLCSMYTPICLEDYKKPLPPCRSVCER-----AKAGCAPLMRQYGFAWPD--RMRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EQPPSGSGHGRP---
                                                                                                                                                                                                                                                                                                                                                                                         Identifying biologically active agents comprises cloning transfected cells into a cell array, exposing the array to an agent to be tested, and detecting signals generated by a reporter molecule as a result of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 0.26;
Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 - PGARPPHRGGGRGGGGGDAAAPPARGGGGGGKAR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 RLPEQGNPDTLCMDYNRTDLTTAAPSPPRRLPPPPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th Similarity 23.7%; Pred. No. 0 51; Conservative 22; Mismatch
                                                     /note= "Encoded by ATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AAAAAALCFAALVAVAVCQG-----
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Fig 66; 90pp; English.
                                                                                                                                                                                                                                                                                           Walsh J;
                                                                                                                                                                         29-APR-2002; 2002WO-GB01946.
                                                                                                                                                                                                                04-MAY-2001; 2001GB-0011004
                                                                                                                                                                                                                                                                                           Andrews P, Draper J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    exposure to the agent
                                                                                                                                                                                                                                                                                                                                WPI; 2003-120579/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                  Key
Misc-difference 434
/no
                                                                                                                                                                                                                                                    (AXOR-) AXORDIA LTD
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                                                                                             WO200290992-A2
                                                                                                                                  14-NOV-2002
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ABUSS 903
ID ABUSS XX
AC ABUSS XX
엄
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ABU55903 standard; Protein; 694 AA

ABUS 5903

Unidentified

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Homo sapiens
    03-OCT-2002
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(first entry)
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from Drosophila and
                                                                                                                                                                                                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL03118.
                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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                                                                                                                                                            Query Match
Best Local S:
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB59015;
                                                                                                                    Sequence
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  8X8888
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                                                                                                                                                                                                                                                                                                                                                                                         요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to modulating the differentiation of an embryonic stem cates the cate of the invention relates to modulating a culture of embryonic stem cells; corporating at least one its active binding fragment.

C stem cell, comprising: (a) providing a culture of embryonic stem cells, comprising is copnate receptor polypeptide expressed by the embryonic stem cells, and the ligand, and (d) growing the cell culture. Also included are:

C are: (i) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a culture comprising embryonic stem cells, comprising: (a) providing a culture feathed with a nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the nucleic acid molecule that hybridises to the mucleic acid molecule sequences of binding a with an embryonic stem cell; (i) and which acid molecule so binding a culture for the maintenance and/or differentiation of embryonic stem cells, comprising the culture for the maintenance and/or differentiation of embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells in an undifferentiated stem; or (3) providing a culture comprising the cell identified in (a) providing a culture comprising the cell sidentified in (a) providing a coluture comprising the cell sidentified in (a) with an endice of (b) or (ii) a molecule subtion are degenerate as a result of the genetic code to the sequences of (i) or (ii), (b) forming a culture comprising the cell identified in (a) which and (b) or cells and (c) growing the culture for the maintenance of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful for treating diseases such as Parkinson's, Huntington's, heart disease,
                                                                                       Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation; ligand; Parkinson's disease; Huntington's disease; motor neuron disease; hart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 72; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gokhale P;
                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001GB-0007296.
23-MAR-2001; 2001GB-0007299.
17-APR-2001; 2001GB-0009346.
                                                                                                                                                                                                                                                                                                                                            25-MAR-2002; 2002WO-GB01195
25-MAR-2003 (first entry)
                                               Human protein Frizzled-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews P, Walsh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-092852/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AXOR-) AXORDIA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABX75330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 KFFLCSMYTPICLEDYKKPLPPCRSVCER-----AKAGCAPLMRQYGFAWPD--RMRCD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 QQLQDVSRECRC----AAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 RIPROGNPDTLCMDYNRTDLTTAAPSPPRRLPPPPPG------EQPPSGSGHGRP--- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
neuron disease, heart disease, diabetes, liver disease (e.g. cirrhosis), renal disease and AlDS (acquired immunodeficiency syndrome). The present sequence is represents a Wht or Notch pathway protein (i.e. a ligand for the method of the invention).
                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA.sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                              -----EVER-ORLRDLOCWOEV
                                                                                                                                                                                                                                                                                                                                                                                                   42 Q-----FRWGTGLRMRCC
                                                                                                                                                                                                                                                                                                 Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila, developmental biology, cell signalling; insecticide, pharmaceutical.
                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3837; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                             ; DB 24; Length 694;
0.26;
thes 72; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 3837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 - PGARPPHRGGGRGGGGDAAAPPARGGGGGGKAR 219
                                                                                                                                                                                                                                                                                                 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                              S AAAAAALCFAALVAVAVÇQG------
                                                                                                                                                                                                                                9.1%; Score 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB59015 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
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48 ACROVLDROLTGGGGGGGGGGGGGGTGLRMGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMP 107
                                                                                                                                                                                                                                   108 PLEKGWWPWGRQQQPPPQGGGGGGGYYYPCSRPG-----EGYGYGQGGQRQMYPPCR 160
                                                                                                                                                                                                      43
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                      Gaps
                                                                                                    9.0%; Score 103.5; DB 22; Length 348; 25.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                          44 PSSGGGGGGG------GGGGGGGGGGGYAAQGGGGGGGGAAAGG
                                                                                                                                  38; Indels
                                                                                                                                    11; Mismatches
                                                                                                                                                                                                    13 ACNATFLSLÍGGGGGGGGGGSK----
                                                                                                                                                                                                                                                                                                       161 PGTTGGGPRIGRVRLTKAREYA 182
                                                                                                                                                                                                                                                                                                                            ---HGGSPQIIKVILQEGQGYS 104
                                                                                                                  Local Similarity 25.49
                                                                     348 AA;
                                                                     Sequence
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                                                                                                    Query Match
                                                                                                                                    Matches
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RESULT 15

ABB62974 standard; Protein; 202 AA. ABB62974; **ABB6297** 

(first entry) 26-MAR-2002

Drosophila melanogaster polypeptide SEQ ID NO 15714.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.

(PEKE ) PE CORP NY.

Li PWD, Venter JC, Adams M,

WPI; 2001-656860/75. N-PSDB; ABL07077.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Disclosure; SEQ ID NO 15714; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence

60 GGGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLE----KGWW 114 115 PWGRQQQPPPQGG----GGGQGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRI 170 Gaps 26; Length 202; Indels 129 RLGGYGNATPQSGKLGYGGQQGGYRRPAPQSGQLYAAGE---48; 9.0%; Score 103; DB 22; 28.3%; Pred. No. 0.1; iive 12; Mismatches 48; Query Match Best Local Similarity 28.33 Matches 34; Conservative 셤 δ 셤

Search completed: November 29, 2003, 17:05:01 Job time : 62 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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using sw model - protein search, OM protein November 29, 2003, 16:58:04; Search time 26 Seconds (without alignments) 761.952 Million cell updates/sec Run on:

score: Title: Perfect

US-10-053-410-4
1148
1 MAKIAAAAAAALCFAALVAV......MMCRLSEPQECSIFSGGDQY Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
Ä	439	38.2	186	~	JC4784	alpha-qlobulin pre
7	435	37.9	186	Н	WMRZ19	19K globulin precu
e.	289.5	25.2	099	7	A24266	glutenin high mole
4	287	25	705	7	S18733	glutenin high mole
S	282.5	~	707	~	852390	D-hordein precurso
9	281	7	648	~	S04832	glutenin high mole
7	157	٦	830	N	S15720	glutenin high mole
80	156	13.6	791	7	JN0690	
σ	156	13.	815	~	B30843	glutenin high mole
10	155.5		848	~	802262	glutenin high mole
11	152	13.2	815	~	JN0689	glutenin, high-mol
12	151.5	13.2	789	7	A30843	glutenin high mole
13	151.5	13.2	838	7	EEWTHW	glutenin, high mol
14	147.5		753	N	JC2099	glutenin, high mol
15	133.5	11.6	191	~	JC4966	high-molecular-wei
16	126		323	N	S38887	2S albumin - commo
17	117.5	10.2	309	7	S10889	proline-rich prote
18	114.5		146	7	S14946	2S seed storage pr
19	114	6.6	297	~	T06500	alpha/beta-gliadin
20	112.5	•	258	-	RZCS	2S seed storage pr
21	112	•	295	~	801062	2S seed storage pr
22	111.5	7.6	307	~	S10015	
23	111	9.7	296	~	807361	alpha/beta-gliadin
24	110	9.6	101	Н	EEWT1	glutenin 1 - wheat
25	110	9.6	139	~	T09878	albumin 2S storage
26	110	9.6	145	7	S13376	CM2 protein - duru
27	110	•	326	7	A41732	heterogeneous ribo
28	110	9.6	386	-	822315	snRNP-associated p
29	109.5	9.5	291	~	T06498	alpha/beta-gliadin

19K globulin precursor - rice N,Alternate names: alpha-globulin C;Species: Oryza sativa (rice) C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 18-Jun-1999 C;Accession: S20024; S25735; PN0497 R;Shorrosh, B.S.; Wen, L.; Zen, K.C.; Huang, J.K.; Pan, J.S.; Hermodson, M.A.; Tanaka, K.

-----RVRLT 158

120 YY-----GGEG-----SSSEQGY-YGEGSSEEGYYGEQQQQPGMT-

g à 셤

177 KAREYAAGLPMMCRLSEPQECSIFSGGDQY 206

RESULT 2

## ALIGNMENTS

9 61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMP-PLEKGWWPWGRQ 119 60 BRFQPWPRRPGALGLRWQCCQQLQDVSRECRCAAIRRWVRSYEESMPWPLEQGWSSSSSE 119 120 QOPPPQGGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMY---PPCRPGTTGGGPRIGRVRLT 176 9 59 A; Accession: JC4784
A; Accession: JC4784
A; Molecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1.186 cARK>
A; Cross-references: DDBJ:D50643; NID:g840704; PIDN:BAA09308.1; PID:g1783206
A; Experimental source: seed
C; Genetics:
A; Gene: G1b
C; Superfamily: wheat alpha-amylase inhibitor
C; Keywords: globulin; seed
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-186/Product: alpha-globulin #status predicted <MAT> 1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG 1 MASKVVFFAAAL-MAAMVAISGAQLSESEMRFRDRQCQREVQDSPLDACRQVLDRQLIGR 28; Query Match 38.2%; Score 439; DB 2; Length 186; Best Local Similarity 51.4%; Pred. No. 1.6e-29; Matches 108; Conservative 20; Mismatches 54; Indels 3 A; Reference number: JC4784; MUID: 96235139; PMID: 8666249 d ò g ò ઠ

9 51

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D-hordein precursor - barley
Cispecies: Hordenu wulgare (barley)
Cispecies: Hordenu wulgare (barley)
Cispecies: Na-May-1995 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
Cispeciesion: S52390; S23921
Risorensen, M.B.; Muller, M.; Simpson, D.
Rubmitted to the EMBL Data Library, February 1995
A;Description: Hordein promoter methylation and transcriptional activity in wild type and
A;Reference number: S52390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glutenin high molecular weight chain 1By9 precursor - wheat C;Species: Triticum aestivum (common wheat)
C;Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S1873
R;Halford, NG;Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.
Theor. Appl. Genet. 75, 117-126, 1987
A;Title: The nucleotide and deduced amino acid sequences of an HWW glutenin subunit gene
                                                                                                                                                                                                                                                                                                                                                   107 PLQQLQQGIFWGTSSQTVQGYYPSVTSPROGSYYPGQASPQQPGQGQQPGKWQEPGQGQQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .---- WGR--- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 MRCCQQLRDVSAKCRPVAVSQVVRQYEQTVVPPKGGSFYPGETTPLQQLQQVIFWGTSSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TVQGYYPSVSSPQQGPYYPGQASPQQPGQQPGKWQELGQGQQGYYPTSLHQSGQGQQG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 YYPCS--RPGEGYGYGYGQG----TTGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YYPSSLQQPGQGQQIGQGQGYYPTSLQQPGQQQIGQGQGYYPTSPQHPGQRQQPGQG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------QQQP------PPQGG------134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LVALTAABGEASRQ----LQCERELQESSLEACRQVVDQQL-----AGRLPWSTGLQ 62
                                                                                                                                                                                                MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG
                                                                       61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 LVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGVGPFRWGTGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-705 <HAL>
A;Cross-references: EMBL:X61026; NID:g22089; PIDN:CAA43361.1; PID:g22090
C;Superfamily: glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.0%; Score 287; DB 2; Length 705; Best Local Similarity 32.9%; Pred. No. 2.38-16; Matches 85; Conservative 24; Mismatches 47; Indels 102;
                                                                                                                                                                                                                                                                                        116 -----WG----WG------RQ-----QQPPPQGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 MRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 YYYPCS--RPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 PRIGR-VRLTKAREYAAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S18733
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A; Status: preliminary
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A; Molecule type: DNA
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A; Residues: 1-660 <THO>
A; Residues: 1-660 <THO>
A; Residues: 1-660 <THO>
A; Residues: 1-660 <THO>
A; Residues: 1-660 <THO>
A; Residues: 1-660 <THO
A; Residues: 1-660 <THO
A; Experimental source: cv. Chinese Spring
B; Goldsbrough, A. P.; Bulleid, N.J.; Freedman, R.B.; Flavell, R.B.
Biochem. J. 263, 837-842, 9842, 9842, 9842, 9842, 9842, 98430; PMID: 2597130
A; Title: Conformational differences between two wheat (Triticum aestivum) 'high-molecula A; Reference number: S06644; MUID: 90088430; PMID: 2597130
A; Accession: S06644
A; Status: not compared with conceptual translation
A; Molecule type: DNA
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C;Species: Triticum aestivum (common wheat)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 20-Aug-1989
C;Accession: A2266; 806644
R;Thompson, R.D.; Bartels, D.; Harberd, N.P.
Nucleic Acids Res. 13, 6833-6846, 1985
Nucleic Nucleotide sequence of a gene from chromosome 1D of wheat encoding a HWW-gluter
A;Reference number: A24266; MUID:86041882; PMID:3840588
                                                                                                                                                                                                                          A, Accession: S25735
A, Molecule type: protein
A, Residues: 66-74108-133,171-186 <SH2>
A, Residues: 66-74108-133,171-186 <SH2>
B, Krishnan, H.B.; Pueppke, S.G.
Biochem Biophyle, Resi Commun. 193, 460-466, 1993
A, Title: Nucleotide sequence of an abundant rice seed globulin: homology with the high A, Reference number: PN0497; MUID:93277591; PMID:8503935
Plant Mol. Biol. 18, 151-154, 1992
A;Title: A novel cereal storage protein: molecular genetics of the 19 kDa globulin of A;Title: A novel cereal storage protein: molecular genetics of the 19 kDa globulin of A;Recession: S20024; MUD:92119226; PMID:1731968
A;Accession: S20024
A;Molecule type: mRNA
A;Residues: 1-186 <SHO>
A;Cross-references: EMBL:X63990; NID:g20158; PIDN:CAA45400.1; PID:g20159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMP-PLEKGWWPWGRQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 YY-----GGEG-----SSSEQGY-YGEGSSEEGYYGEQQQQPGMT-----RVRLT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERFOPMFRRPGALGLRMOCCOOLODVSRECRCAAIRRMVRSYEESMPMPLEQGWSSSSSE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 QQPPPQGGGGGGGYYYPCSRPGEGYGYGQGGQRQMY---PPCRPGTTGGGPRIGRVRLT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.9%; Score 435; DB 1; Length 186; Best Local Similarity 51.0%; Pred. No. 3.4e-29; Matches 107; Conservative 20; Mismatches 55; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: PN0497
A,Molecule type: mRNA
A,Rosidues: ARIA
A,Cross-references: GB:L12252
A,Experimental source: geed
C,Superfamily: wheat alpha-amylase inhibitor
C,Keywords: storage protein
C,Stay B, 222/Domain: signal sequence #status predicted <SIG>F;1-224/Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.2%; Score 289.5; DB 2; 36.2%; Pred. No. 1.4e-16; ive 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.2
Best Local Similarity 36.2
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
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13,

A,Residues: 1-475 <sor> A;Cross-references: EMBL.X84368; NID:g671536; PIDN:CAA59104.1; PID:g671537 B;Halford, N.G.; Tatham, A.S.; Sui, E.; Daroda, L.; Dreyer, T.; Shewry, P.R. Biochim. Biophys. Acta 1122, 1992 Biochim. Biophys. Acta 1122, 1992 A;Title: Identification of a novel beta-turn-rich repeat motif in the D hordeins of barl A;Reference number: S23921; MUID:92353095; PMID:1643086 A;Accession: S23921 A;Residues: 267-355, P',357-359, Q',361-458, Y',460-707 <hal> A;Residues: 267-355, P',357-359, Q',361-458, Y',460-707 <hal> A;Cross-references: EMBL:X68072; NID:g18969; PIDN:CAA48209.1; PID:g18970 C;Genetics: A;Gene: hor3 G;Superfamily: glutenin</hal></hal></sor>	
C; Keywords: seed; storage protein F;12-21/Domain: signal sequence #status predicted <sig> F;22-707/Product: D-hordein #status predicted <mat> Query Match  Query Match  Con 28:5; DB 2; Length 707;</mat></sig>	RESULT 7 315720 315727 glutenin high molecular weight chain 1Ax1 precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 08-Jun-11994 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
	C;Accession: \$15720 R;Halford, N.G.; Field, J.M.; Blair, H.; Urwin, P.; Moore, K.; Robert, L.; Thompson, R.; submitted to the EMBL Data Library, July 1991 A;Description: Analysis of HMW glutenin subunit encoded by chromosome 1A of bread wheat: A;Reference number: \$15720
OY 55 RQLTGGGGGGGVGPFRWGTGLRWRCCQQLQDVSRECRCAAIRSMVRGYEE 104	A;Secture: preliminary A;Molecule type: DNA A;Residues: 1-830 <hal> A;Residues: 1-830 <hal> C;Superfamily: allowed: NID:g21742; PIDN:CAA43331.1; PID:g21743 C;Superfamily: qlutenin</hal></hal>
105PWGRQQQPPPQGGGGGGGGYY	Query Match 13.7%; Score 157; DB 2; Length 830; Best Local Similarity 24.6%; Pred. No. 1.7e-05; Matches 63; Conservative 17; Mismatches 42; Indels 134; Gaps 11;
OY 139 5	QY 11 ALCFAALVAVAVCGGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGGFFR 70
RESULT 6 \$04832 glutenin high molecular weight chain (Dy10) - wheat C.Species: Triticum aestivum (common wheat) C.Species: Preb-1990 #sequence_revision 28-Peb-1990 #text_change 20-Aug-1999	Oy 71 WGTGLRWRCCQOLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWP
R.E.; Halford, N.G.; Shewry, P.R.; Malpica	
A/IILIE: NUCLEOLIDE BEQUENCES OF The Two nign-molecular-weight glutenin genes from the D A/Reference number: S02262; MUID:89098419; PMID:2563152 A/RACCESSION: S04832 A/RACLES NOT Compared with conceptual translation A/Molecule type: DNA	OY 128 GGGGGGY150  Db 159 GGGGAXYPTSPQGGGGPGYYPTSPWQPEQLQQPTGGQQRQQFGQGQGCGC 150  CV 151GAROWYPPCRPG 162
gl360617; PIDN:CAA31396.1; PID:g21751 Freedman, R.B.; Flavell, R.B.	219 GQGQPRYYPTSSQQPG
Affitle: Conformational differences between two wheat (Triticum aestivum) 'high-molecula A;Reference number: S06644; MUID:90088430; PMID:2597130 A;Accession: S06645 A;Accession: S06645 A;Status: not compared with conceptual translation A;Molecule type: DMA A;A;Molecule type: DMA A;A;Molecule type: DMA A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A	RESULT 8 JN0690 JUN0690 JULOHIA, high-molecular-weight Bx7 chain precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994
Cigenetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: Cisuperfamily: glutenin	CyAnderson, Owoso, O.D.; Greene, F.C. Theor. Appl. Genet. 77, 689-700, 1989 Affile: The characterization and comparative analysis of high-molecular-weight glutenin A.Peference number: HAMES
Query Match  Query Match  Best Local Similarity 36.6%; Pred. No. 6.88-16;  Matches 78; Conservative 23; Mismatches 46; Indels 66; Gaps 11;  Qy I MAKIADADALCFAALVAVAVQGEVERQELEDLQCREVELDARQVLDRQLTGG 60	AACCESSION: JN0690 A,MOLECULE type: DNAA A,MOLECULE type: DNAA A,Residues: 1-791 cAND> C,Comment: The main wheat storage proteins are divided into two groups. The glutenins, cc a families. C,Superfamily: glutenin C,Keywords: seed; storage protein C,Keywords: seed; storage protein F;1-21/Domain: signal sequence #status predicted <sig></sig>

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A,Accession: JN0689
A,Molecule type: DNDA
A,Residues: 1-815 <ANDA
A,Note: the authors translated the codon CTA for residue 11 as Val, CAT for residue 496 ¢
C,Comment: The main wheat storage proteins are divided into two groups. The glutenins, cc
a families:
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiAnderson, O.D.; Greene, F.C.
Theor. Appl. Genet. 77, 689-700, 1989
A;Title: The characterization and comparative analysis of high-molecular-weight glutenin
A;Reference number: JN0689
Nucleic Acids Res. 17, 461-462, 1989
A,Title: Nucleotide sequences of the two high-molecular-weight glutenin genes from the
A,Reference number: S02262, MUID:89098419, PMID:2563152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: glutenin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-815/Product: glutenin, high-molecular-weight Ax2* chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 TGGGGGGGGGGGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------RQQQPPPQG--GGGGQGGY- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 GETTPPQQLQQRIFWGIPALLKRYYPSVTCPQQVSYYPGQASPQRPGQGQQPGQGQGYY 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 Y------YYPCS-----GQRQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 YYPTSPQQSGQKQPGYYPTSPWQPEQLQQPTQGQQRQQPGQGQQLRQGQGQQGQGGQGPR 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutenin, high-molecular-weight Ax2* chain precursor - wheat
C,Species: Triticum aestivum (common wheat)
C,Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 15-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                   52 -------QQLRDISPECHPVVVSPVAGQYEQQIVVPPKGGSFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGVGPFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 -------YYPCS-----RPGEGYGYGQGGQRQMYPPCRPG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PISPQQPGQWQQPEQGQPRXYPTSPQSGQLQQPAQGQQPGQGQQPGQGQPG
                                                                                                                                                                                                                                                                                                                        Indels 105;
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                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                      13.5%; Score 155.5; DB 2; 26.0%; Pred. No. 2.3e-05; tive 17; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 13.2%; Score 152; DB 2; Best Local Similarity 24.4%; Pred. No. 4.4e-05; Matches 61; Conservative 18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 -------WG------
                                                                          A,Accession: S02262
A,Molecule type: DNA
A,Residues: 1-848 <AND>
A,Cross-references: EMBL:X12928
C,Genetics:
A,Gene: Glu-Dl-1b
C,Superfamily: glutenin
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.0%
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 -WG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: JN0689
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glutenin high molecular weight chain Dx5 - wheat
C;Species: Triticum aestivum (common wheat)
C;Bate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 03-Feb-1994
C;Accession: S02262
R;Anderson, O.D.; Greene, F.C.; Yip, R.E.; Halford, N.G.; Shewry, P.R.; Malpica-Romero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glutenin high molecular weight chain Ax2 precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Species: Triticum aestivum (common wheat)
C;Species: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C;Accession: B30843
R;Anderson, O.D.; Greene, F.C.
submitted to GenBank, January 1989
A;Reference number: A94515
A;Accession: B30843
A;Molecule type: DNA
A;Residues: 1-815 <AND
C;Superfamily: glutenin
C;Keywords: seed; storage protein
C;Keywords: seed; storage protein
F;1-21/Domain: signal sequence #status predicted <&IG>F;2-815/Froduct: glutenin Ax2 chain #status predicted <WAT>F;2-815/Froduct: glutemine/glycine/proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 YYPTSPQQSGQKQPGYYPTSPWQPEQLQQPTQGQQRQQPGQGQQQLRQGQQGQGQGQPR 218
                                                                                                                                                                                                                                                  61 GGGGGVGPFRWGTGLRAMRCCQQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWP--- 115
                                                                                                                                                                                                                                                                                                                                              -----PPQGGGGGGYYYPCSRPGE 143
                                                                                                                                                                                                                                                                                                                                                                                           84 TPSQQLQQMIFWGIPALLRRYYPSVTSSQQGSYYPGQASPQQSGQQPGQE---QQPGQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 WGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWP------- 115
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       ?;22-791/Product: glutenin, HMW Bx7 chain #status predicted <MAT>
                                                      DB 2; Length 791;
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A; Title: Construction and expression of a synthetic wheat storage protein gene.
A; Reference number: JC4966; MUID:97017127; PMID:8863728
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A;Accession: JC4966
A; Molecule type: DNA
A;Residues: 1-161 <and></and>
A, Note: the authors translated the codon GAT for residue 12 and GAC for residue 31 as Gl
C, Comment: This protein belongs to one class of wheat prolamines.
C;Superfamily: glutenin

clearing : Errmannia											
Query Match	atch	Query Match 11.6%; Score 133.5; DB 2;	11.6%;	Score	11.6%; Score 133.5; DB 2; Length 161;	DB 2;	Length	161;			
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Ov 133 GYYYPCSRPGEGYGYGOGGOROMYPPCRPGTTGGGPRI-----GRVRLTKAREYAAGLP 186

Search completed: November 29, 2003, 17:07:05 Job time: 29 secs

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Length 186;

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CHAIN SEQUENCE Query Match

P04729 triticum ae P10496 phaseolus v Q01844 homo sapien P28041 hordeum vul P19470 schistosoma P80136 avena sativ PQ1085 triticum ae P80198 hordeum vul P4311 sinapis alb P8405 rattus norv Q92125 xenopus lae	PRT; 186 AA.  ted) sequence update) annotation update) (Alpha-globulin). Streptophyta; Embryophyta; Tracheophyta; tta; Liliopsida; Poales; Poaceae;	.K., Pan J.S., Hermodson M.A., ar genetics of the 19 kDa	globulin: homology with rye and triticale."; 93).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	NIT.  1. TENTIAL.  kpa GLOBULIN. 9E09BA74CB0B6810 CRC64;
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                                                                                                                         61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMP-PLEKGWWPWGRQ 119
                                                                                                                                               60 ERFQPMFRRPGALGLRMQCCQQLQDVSRECRCAAIRRMVRSYEESMPMPLEQGWSSSSSE 119
                                                                                                                                                                                                                             120 YY-----GGEG-----SSSEQGY-YGEGSSEEGYYGEQQQQPGMT-----RVRLT 158
                                                                                                                                                                                             120 QQPPPQGGGGGGGYYYPCSRPGEGYGYGQGGQRQMY---PPCRPGTTGGGPRIGRVRLT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HWY-glutenin subunit.";

Nucleic Acids Res. 13:6833-6846(1985).

-- FUNCTION: GLUTENINS ARE THE HIGH WOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-- SUBUNIT: DISULIPLE -- BRIDGE LINKED AGREGATES.
-- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP I CHROMOSOMES OF WHEAT.
-- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                          1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Chinese Spring;
MEDIINE=86041882; bubMed=3840588;
Thompson R.D.; Bartels D.; Harberd N.P.;
"Nucleotide sequence of a gene from chromosome 1D of wheat encoding a
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticeae, Triticum.
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                  28;
                Indels
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit 12 precursor.
51.0%; Pred. No. 7.7e-28; ive 20; Mismatches 55;
                                                                                                                                                                                                                                                                KAREYAAGLPMMCRLSEPQECSIFSGGDQY 206
                                                                                                                                                                                                                                                                                    :||:||| || |||: |||:|||: |||
159 RARQYAAQLPSMCRV-EPQQCSIFAAG-QY 186
                                                                                                                                                                                                                                                                                                                                                                                        660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         , Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@igb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03157; Glutenin hmw; 1. PRINTS; PR00210; GLUTENIN. SMART; SM00499; AAI; 1.
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70868 MW;
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01-AUG-1988 (Rel. 08, Last seq
15-JUL-1999 (Rel. 38, Last ann
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InterPro; IPR001419; Glutenin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (Wheat).
Best Local Similarity 51.0
Matches 107; Conservative
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660 AA;
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SEQUENCE
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GLT3_WHEAT
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                                                                                                                                                                     107 PLQQLQQGIFWGTSSQTVQGYYPSVTSPRQGSYYPGQASPQQPGQQQQPGKWQEPGQGQQ 166
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                                                                          1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG
                                                                                               61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Cheyenne; MEDLINE=89088419; PubMed=2563152; Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R., Malpica-Romero J.M.; "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROUP I CHROMOSOMES OF WHEAT.
-!- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE
NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
     Length 660;
25.2%; Score 289.5; DB 1; Length 36.2%; Pred. No. 7.8e-16; . ive 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF03157; Glutenin hmw; 1.
PRINTS, PR00210; GLUTENĪN.
SMART; SM0499; AAI, 1.
Seed storage protein; Repeat; Multigene family; Signal.
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01-MAR-1989 (Rel. 10, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit DY10 precursor.
                                                                                                                                                                                                                                                                                                 134 YYYPCS--RPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                   167 WYYPTSLQQPGQQIGKG--KQGYYPTSLQQPGQQQGQ
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                                      80; Conservative
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   Query Match
Best Local Similarity
Matches 80; Conserv
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GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT

IPR001419; Glutenin.

Length

89359 MW; 0F14E1106D552643 CRC64;

REPEATS

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Seed storage protein; Repeat; Multigene family; Signal
                          Pfam; PF03157; Glutenin hmw; 1. PRINTS; PR00210; GLUTENIN.
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Best Local Similarity 28.1%
Matches 59; Conservative
InterPro;
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GLT4_WHEAT
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                                                                                                                                                                                                                                                                                                                                         61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP---- 115
                                                                                                                                                                                                                                                                                                                                                                                52 ----AGRLPWSTGLQMRCCQQLRDVSAKCRSVAVSQVARQYBQYEQTVVPPRGGSFYPGETT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 PLQQLQQGIFWGTSSQTVQGYYPGVTSPRQGSYYPGQASPQQPGQGQQPGKWQEPGQGQQ 166
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SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
RISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP I CHROMOSOMES OF WHEAT.
MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQOPGQ AND
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
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MEDLINE=89098419; PubMed=2563152;
Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.
Malpica-Romero J.M.;
                                                                                                        'Match 24.5%; Score 281; DB 1; Length 648; Local Similarity 36.6%; Pred. No. 3.6e-15; les 78; Conservative 23; Mismatches 46; Indels
                             610 REPEATS.
69629 MW; FE98F1D44B9E9AF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit DXS precursor.
GLU-1D-1D OR GLU-D1-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 WYYPTSLQQPGQQQIGK-GQQGYYPTSLQQPG 198
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648 AA;
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                                                                                                                                                                               58 TGGGGGGGGGGPRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWP 115
                                                                                                                                                                                                                                                                    -----RQQQPPPQGGGGGGY-YY 136
                                                                                                                                                                                                                                                                                                              89 GETTPPQQLQQRIFWGIPALLKRYYPSVTCPQQVSYYPGQASPQRPGQGQQPGQGQGYY 148
                                                                                       57
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                                                                                                                                   21
                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANBOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                       1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQC---WQEVQESPLDACRQVLDRQL
                                                                                                                                 1 MAKRIVLFVAVV--VALVALTVAEGEASEQ----LQCERELQELQERELKACQQVMD---
                                                                                                                                                                                                        52 ---------QQLRDISPECHPVVVSPVAGQYEQQIVVPPKGGSFYP
                                           81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acide Res. 13:8729-8737(1985).

-1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

-1- SUBUNIT: DISULPIDE-BRIDGE LINKED AGGREGATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Yamhill;
MEDLINE=8603674; PubMed=3001648;
SUGIVAMA T., Rafalski A., Peterson D., Soll D.G.;
"A wheat HWW glutenin subunit gene reveals a highly repeated
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P08489;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit PW212 precursor.
Triticum aestivum (Wheat).
13.6%; Score 156.5; DB 1; 28.1%; Pred. No. 3.1e-05; ive 20; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838 AA.
                                                                                                                                                                                                                                                                                                                                                            137 PCS--RPGEGYGYGQGGQRQMYP--PCRPG 162
                                                                                                                                                                                                                                                                                                                                                                                                   149 PISPOOPGO-WEEPEOGOOGYYPISPOOPG 177
                                                                                                                                                                                                                                                                    116 ------WG-----
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InterPro; IPR001419; Glutenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X03346; CAA27052.1; -. PIR; A24107; EEWTHW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHEAT
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EMBL; X12928; CAA31395.1; -.

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                                                                                                                                                                                                                                                                                                                                            PIR; A25802; A25802.

PIR; S14946; S14946.

PIR; JGAS; 30-APR-0.

InterPro; IPR003612; AAI.

InterPro; IPR003617; Napin.

Pfam; PF00234; Lryp, alpha_amyl; 1.

PRINTS; PR00499; AAI; 1.

Seed storage protein; Signal; Allergen; Pyrrolidone carboxylic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                 .i. SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 146;
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I -> L (IN REF. 4).
A7DF778FD766410D CRC64;
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EE -> QQ (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-199 (Rel. 38, Last annotation update)
15-Dha/beta-gliadin A-IV precursor (Prolamin).
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Okita T.W., Cheesbrough V., Reeves C.D.;
                                                                                                                                                                                                                                                                                                            EMBL; X54491; CAA38363.1; ALT_SEQ.
EMBL; A13818; CAA01131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16911 MW;
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Best Local Similarity 28...,
Best Local Similarity 28...,
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Eukaryota, Viridiplantae;
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                                                                                                                                                                                                                                                X57027;
X57028;
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SIGNAL
PROPEP 2
CHAIN 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AMPPLEKGWWP--WGRQQ-----QPPPQGGGGGGGGGYYYPCSRPG 142
                                                                                                                                                                                                                                                                                                                                                                          ---- 104
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                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQC---WQEVQESPLDACRQVLDRQL
                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                    Gaps
                                                                                                    GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91370890; PubMed=1840683;
Gander E.S., Holmstroem K.O., de Paiva G.R., de Castro L.A.B.,
Carneiro M., Grossi de Sa M.F.;
"Isolation, characterization and expression of a gene coding for a
albumin from Bertholletia excelsa (Brazil nut).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2S sulfur-rich seed storage protein precursor (Allergen Ber e 1) BE2S1 AND BE2S2.
                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                         13.2%; Score 151.5; DB 1; Length 838; 28.7%; Pred. No. 7.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Lecythidaceae; Bertholletia.
                                                                                                                                                                                                                                                                                                                                                                          58 TGGGGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE-
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Submitted (DEC-1990) to the EMBL/GenBank/DDBJ databases
Pfam; PF03157; Glutenin hmw; 1.
PRINTS; PR00210; GLUTENIN.
Seed storage protein; Repeat; Multigene family; Signal.
SIGNAL
                                                                                                                                                                 71D715B7BDF0722D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P044_03; P04402;
20-MAR-1987 (Rel. 04, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA
                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                             REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 QGQQSGQ-GQQGYYPTSPQQPG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertholletia excelsa (Brazil nut)
                                                                                                                                                                 838 AA; 89174 MW;
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                                                                                                                                                                                                                                                  58; Conservative
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SEQUENCE
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGSF----QPSQQNPQAQGSVQPQQLP------QFEEIRNLALETLPAM 277
                                                                                                                                                                                                                                                                                                                                                                                                                                             83
         gliadin DNA sequences.";
J. Biol. Chem. 266:8203-8213(1985).
-!- FUNCTION: GLIADIN IS THE MAJOR SEED STORAGE PROTEIN IN WHEAT.
-!- MISCELLANEOUS: THE ALPHA/BETA-GLIADINS CAN BE DIVIDED INTO 5
HOWOLOGY CLASSES. SEQUENCE DIVERGENCE BETWEEN THE CLASSES IS DUB
TO SINGLE BASE SUBSTITITIONS AND TO DUPLICATIONS OR DELETIONS
WITHIN OR NEAR DIRECT REPEATS. THERE ARE MORE THAN A 100 COPIES OF
THE GENE FOR ALPHA/BETA-GLIADIN PER HAPLOID GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 WQIPEQSRCQAIHNVVHAIILHQQQQQQQQQQQQQQPLSQVCFQQSQQQYP----SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Irwin S.D., Keen J.N., Findlay J.B.C., Lord J.M.;
"The Ricinus communis 2S albumin precursor: a single preproprotein
may be processed into two different heterodimeric storage proteins.";
Mol. Gen. Genet. 222:400-408 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
"Evolution and heterogeneity of the alpha-/beta-type and gamma-type
                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis (Castor bean).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Euphorbiacae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                       Match 9.9%; Score 114; 'DB 1; Length 297; Local Similarity 23.0%; Pred. No. 0.026; Gonservative 29; Mismatches 76; Indels 4
                                                                                                                                                                                                                                                                                                                        Seed storage protein; Repeat; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                  ALPHA/BETA-GLIADIN A-IV.
0025ED289AE9588B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
25 albumin precursor (Allergen Ric c 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AA.
                                                                                                                                                                                                                                                    InterPro; IPR003612; AAI.
InterPro; IPR001954; Glia_glutenin.
                                                                                                                                                                                                                                                                                   Pfam; PF00234; tryp alpha amyl; 1. PRINTS; PR00208; GLIADGLUTEN. SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Endosperm;
MEDLINE=91109729; PubMed=2274038;
                                                                                                                                                                                                                                                                                                                                                              34239 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDVSRECRCAAIRSMVRG---
                                                                                                                                                                                                                                 EMBL; M11075; AAA34282.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 CRLSEPQECSI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNVYIPPYCTI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                              297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2SS_RICCO
P01089:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ID 2SS_R
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CERYLRQSSSRRSPGEEV-----LRMPGDENQQQESQQLQQCCNQVKQVRDECQCEA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blochem, J. 213:543-545[1983].
-1- FUNCTION: THIS IS A 2S SEED STORAGE PROTEIN.
-1- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AALVAVAVCQGEVERQRLRDLQCWQEVQESPLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKLIPTIALVSVLLFIIANASPAYRTTITTEIDESKGEREGSSSQOCROEVQRKDLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 CRQVLDRQLTGGGGGGGGGGGGGGGTRM-------RCCQQLQDVSRECRCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 IRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGGYYYPCSR-----PGEGYGYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Allergen; Pyrrolidone carboxylic acid. PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83308577; PubMed-6615448;
Odani S., Koide T., Ono T., Ohnishi K.;
"Structural relationship between barley (Hordeum vulgare) trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINKED BY 2 DISULFIDE BONDS.
--- PTM: THE TWO DISULFIDE BONDS LINKING THE SMALL AND THE LARGE CHAINS INVOLVE CYS-162 AND CYS-175.
--- SIMILARITY: BELONGS TO THE 28 SEED STORAGE ALBUMINS FAMILY.
                                                                                                                                                                                                                     MEDLINE-83082772; PubMed=7174664; Sharief F.S., Li S.S.-L.; "Amino acid sequence of small and large subunits of seed storage
                                                    Irwin S.D., Lord J.M.;
Nucleotide sequence of a Ricinus communis 2S albumin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor and castor-bean (Ricinus communis) storage protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2S ALBUMIN, LARGE CHAIN.
PYRROLIDONE CARBOXYLIC ACID
E -> Q (IN REF. 3).
MISSING (IN REF. 3).
D -> N (IN REF. 3).
E -> Q (IN REF. 3).
W, 27874CFC50E41072 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2S ALBUMIN, SMALL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                      Nucleic Acids Res. 18:5890-5890(1990)
                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 257:14753-14759(1982).
                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY TO PROTEINASE INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00234; tryp_alpha_amyl; 2.
PRINTS; PR00496; NAPTN
SMART; SM00499; AAI; 1.
Seed storage protein; Signal; Alle
TISSUE=Endosperm;
MEDLINE=91016940; PubMed=2216785;
                                                                                                                                                                                             SEQUENCE OF 157-190 AND 194-258
                                                                                                                                                                                                                                                                                                            protein from Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X54158; CAA38097.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
223
223
234
255
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255 2
258 AA;
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WHEAT
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                                                                                                             P18573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                  WHEAT
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GDA6_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 QCWQEVQESPLDACRQVLDRQLTGGGGGGGVGPFRWG-----TGLRMRCCQQLQDVSRE 89
166 IQEQQNLRQCQEYIKQQVSGQGPRRSDNQERSLRGCCDHLKQMQSQCRCEGLRQAIEQQQ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 ÓCRETEIQRPVGECQRFVEQÓMQOSPRSTRPYQQRPGQQQQQQGRGLQQQCCNELQNVKKE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRCAAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, campanulids, Asterales, Asteraceae, Asteroideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 GGQRQMYPPCRPGTTGGGPRIGRVRLTKAREYAAGLPMMCRLSEPQECSIFSG 202
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                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 14) Last annotation update)
28 seed storage protein precursor (2s albumin storage protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Cv. Giant grey stripe;
MEDLINE=88142538; PubMed=2830455;
Allen R.D., Cohen B.A., Vonder Haar R.A., Adams C.A., Ma D.P.,
Nessler C.L., Thomas T.L.;
"Sequence and expression of a gene encoding an albumin storage
protein in sunflower.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHCEAIQEVARRVMRQ-------PQQQQQRRGQFGGQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2S SEED STORAGE PROTEIN.
8958A106805142A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seed storage protein; Signal; Multigene family.
                                                                    -IGRVR---LTKAREYAAGLPMMCRLSEPQEC 197
                                                                                                        226 SQGQLQGQDVFEAFRTAANLPSMCGVS-PTEC 256
                                                                                                                                                                                                                                 295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 162-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                              (Common sunflower)
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00234; tryp_alpha_amyl; 2. SMART; SM00499; AAI; 2.
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                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heliantheae; Helianthus
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Helianthus annuus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4232;
                                                                                                                                                                                                                                 HELAN
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                                                                                                                                                                                                                                   2SS5 HEI
P15461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ODVSRECRCAAIRSMVRG-----YEEAMPPLEKGWWPWGRQQQPPPQGGGGGGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 WOIPEQSRCQAIHNVVHAIILHQQQQQQQQQQQQPLSQVSFQQPQQQYP----SGQGS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 YYYPCSRPGEGYGYGQGG-QRQMYPPCRPGTTGGGPRIGRVRLTKAREYA-AGLPMMCRL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 F----QPSQQNPQAQGSVQPQQLP-------QFEEIRNLALETLPAMCNV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcia-Marcto F., Manana C., Garcia-Olmedo F., Carbonero P.;
"Nucleotide sequence of a cDNA encoding an alpha/beta-type gliadin
from hexalloid wheat (Triticum aestivum).";
Plant Mol. Biol. 14:867-868(1990).
-!- FUNCTION: GLIADIN IS THE MAJOR SEED STORAGE PROTEIN IN WHEAT.
-!- FUNCTION: GLIADIN IS THE MAJOR SEED STORAGE PROTEIN IN WHEAT.
-!- MISCELLANEOUS: THE ALPHA/BETA-GLIADINS CAN BE DIVIDED INTO 5
HOMOLOGY CLASSES. SEQUENCE DIVERGENTEEN THE CLASSES IS DUE
TO SINGLE BASE SUBSTITUTIONS AND TO DUPLICATIONS OR DELETIONS
WITHIN OR NEAR DIRECT REPEATS. THERE ARE MORE THAN A 100 COPIES OF
THE GENE FOR ALPHA/BETA-GLIADIN PER HAPLOID GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 QGEVERQRIRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGGFRWGTGLRMRCCQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Gaps
                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 9.7%; Score 111.5; DB 1; Length : Similarity 23.4%; Pred. No. 0.043; 44; Conservative 29; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed storage protein; Repeat; Signal; Multigene family
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                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Alpha/beta-gliadin MMI precursor (Prolamin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Chinese Spring; TISSUE=Endosperm;
MEDLINE=91346679; PubMed=2102865;
307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X17361; CAA35238.1; -.
PIR; S10015; S10015.
InterPro; IPR003612; AAI.
InterPro; IPR01954; Glia_glutenin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00208; GLIADGLUTEN.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA; 35397 MW;
                                                                                                                                                                                                                                           Triticum aestivum (Wheat)
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-53
                                                      NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHEAT
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 QQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHINAHARSQVLQQSTYQPLQQLCCQQL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 QDVSRECRCAAIRSMVRG---YEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYYYPCSR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PQQQYPSGQG----FFQPSQQNPQAQGSVQPQQLPQFEEIRNLALQT----LPRMCNVYI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 PGEGYGYGOGGOROMYPPCRPGTTGGG-----PRIGRVRLTKAREYAAGLPMMCRLSE 193
                                                                                                                       24 QGEVERQRIRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGPFRWGTGLRMRCCQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA/BETA-GLIADIN CLONE PW1215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.7%; Score 111; DB 1; Length 296; Best Local Similarity 23.2%; Pred. No. 0.045; Matches 43; Conservative 26; Mismatches 76; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                       Seed storage protein; Repeat; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 296 AA; 33941 MW; A9BDF590AD40F135 CRC64;
                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Alpha/Deta-gliadin clone PW1215 precursor (Prolamin).
Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
  296 AA.
                                                                                                                                                                                                                                                                                                                                                        PIR; S07361; S07361.
InterPro; IPR003612; AAI.
InterPro; IPR001954; Glia_glutenin.
Pfam; PF00224; LYYP alpha amyl; 1.
PRINTS; PR00208; GLIADGLUTEN.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                       EMBL; X02538; CAA26383.1; -. EMBL; K03074; AAA34277.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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30,
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(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 PPYCS 284
                                                                                                        NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLT1 WHEAT
P02861;
21-JUL-1986
21-JUL-1986
01-OCT-1994
GDA6 WHEAT P04726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
GLT1_WHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ĠQGQQPRQWLQPRQGQQG----YYPTSPQQSGQGQQLGQG--QQGYYPTSPQQSGQQQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-i- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-i- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Gaps
                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Forde J., Forde B.G., Fry R.P., Kreis M., Shewry P.R., Miflin B.J.;

"Identification of barley and wheat cDNA clones related to the high-
M-r polypeptides of wheat gluten.";

FEBS Lett. 162:360-366(1983).

-I. FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, Pooldeae, Triticeae, Triticem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
Alpha-amylase/trypsin inhibitor CM2 precursor (Chloroform/methanol-soluble protein CM2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gautier M.F., Alary R., Iullien V., Joudrier P.,
"Nucleotide sequence of a cDNA clone encoding the wheat (Triticum
durum Desf.) CM2 protein.";
Plant Mol. Biol. 16:333-334(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 ------RIGRVRLTKAREYAAGLPMMCRLSEPQECSIFSGGD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.6%; Score 110; DB 1; Length 101; Il Similarity 33.3%; Pred. No. 0.02; 36; Conservative 11; Mismatches 25; Indels
Glutenin, high molecular weight subunit PC256 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA; 10896 MW; EF6D6ADDDFEED993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed storage protein; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GYDSPYHVSAEHQAASLKVAKAQQLAAQLPAMCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Agathe; TISSUE=Seed; MEDLINE=91370875; PubMed=1893104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03157; Glutenin hmw; 1. PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001419; Glutenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X00054; CAA24933.1; -. PIR; A03352; EEWT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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MEDLINE=92112968; PubMed=1730754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
               Matunis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haynes S.R., Johnson D., Raychaudhuri G., Beyer A.L.; "The Drosophila Hrb87F gene encodes a new member of the A and B hnRNP
                                                                                                               QUALITY OF PASTA.
SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR
                                                                                                                                                                                                                                                                                      InterPro; IPR003612; AAI.
InterPro; IPR006105; Try/amyl_inhib.
Pfam, PF00234; tryp_alpha_amyl; 1.
PR00499; AAI; 1.
PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
Serine protease inhibitor; Alpha-amylase inhibitor; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Barber D., Sanchez-Monge R., Garcia-Olmedo F., Salcedo G., Mendez E. "Evolutionary implications of sequential homologies among members of the trypsin / alpha-amylase inhibitor family (CM-proteins) in wheat
                                                 Biochim. Biophys. Acta 873:147-151(1986).
-!- FUNCTION: ALPHA-AMYLASE/TRYPSIN INHIBITOR. IT COULD BE INVOLVED
IN INSECT DEPENSE MECHANISMS.
-!- TISSUE SPECIFICITY: DEVELOPING ENDOSPERM.
-!- TISSUE SPECIFICITY: MOULD BE INVOLVED IN THE COOKING
                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-AMYLASE/TRYPSIN INHIBITOR CM2.
8A6C95C1DF88940C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Heterogeneous nuclear ribonucleoprotein 877F (HRP36.1 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 110; DB 1; Length 145; 27.4%; Pred. No. 0.028; at:ive 13; Mismatches 34; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPVSTEPGNTPRDRCCKELYDASQHCRCEAVRYFI 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Oregon-R, and Canton-S; TISSUE=Ovary;
MEDLINE=91187645; PubMed=1849257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein group.";
Nucleic Acids Res. 19:25-31(1991)
                                                                                                                                                                                                                                                                                                                                                                                                      145 AA; 15460 MW;
                                                                                                                                                                                                                                                                 EMBL; X55454; CAA39099.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 27.4 tes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRB87F OR HRP36.
                                     barley.";
                                                                                                                                                                                                                                                                                                                                                                   Signal
                                                                                                                                         FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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P48810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 ---GDŘGQGGG------GWGGQNRQNGGGNWGGAGGGGGFGNSGGNFGGGQGGGSG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 LOCWOEVQESPLDA----CRQVLDRQLTGGGGGGGGGGGGGGELRMGTGLRMRCCQQLQDVSREC 90
                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.
-1- SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUE=Embryo;
MEDLINE=92020124; PubMed=1717937;
Hovemann B.T., Dessen E., Mechler H., Mack E.;
"Drosophila snRNP associated protein P11 which specifically binds to heat shock puff 93D reveals strong homology with hnRNP core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2; Synonyms=HRP36.1;
ISOId=P46810-2; Sequence=VSP_005807;
-!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
Matunis B.L., Matunis M.J., Dreyfuss G.; "Characterization of the major hnRNP proteins from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM RNP 1; 2.
RNA-binding; Nuclear protein; Ribonucleoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2036C04D01E3AFD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0030529; C:ribonucleoprotein complex; IDA.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP 005807.
S -> T (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Sco. No. v. 29.7%; Pred. No. v. 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P48810-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 19:4909-4914(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005717; C:chromatin; IDA.
GO; GO:0016607; C:nuclear speck; IDA.
                                                                                    Cell Biol. 116:257-269(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOROMYPPCRPGTTGGGP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0004237; Hrb87F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54803; CAA38574.1; -. EMBL; X62636; CAA44502.1; -. EMBL; X59691; CAA42212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A41732; A41732.
PIR; S22315; S22315.
HSSP; P09651; 1UP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing
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315
                                                              melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 GQGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGRVRLTKAREYAAGLPMMC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 QDVSRECRCAAIRSMVRG------YEEAMPPLEKGWWPWGRQQQPPPQGGGG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 ---GFFQPSQQNPQAQGSFQPQQL-------PQFEEIRNLALQT----LPAMC 272
                                                                                                                                                                                                                                                                                                                24 QGEVERORLRDLQCWQEVQESPLDACROVLDRQLTGGGGGGGGGGGFRWGTGLRMRCCQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                     MEDLINE=85234522; PubMed=2989281;
Okita T.W., Cheesbrough V., Reeves C.D.;
"Evolution and heterogeneity of the alpha-/beta-type and gamma-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.5%; Score 109.5; DB 1; Length 291; 21.6%; Pred. No. 0.058; tive 30; Mismatches 80; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003612; AAI.
InterPro; IPR001954; Glia_glutenin.
Prem; Pr00224; tryp_alpha_amyl; 1.
PRINTS; PR00228; GLIADGLUTEN.
SWART; SMO0499; AAI; 1.
Seed storage protein; Repeat; Signal; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA/BETA-GLIADIN A-II. 9B39F93B0825A2E0 CRC64;
                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Alpha/beta-gliadin A-II precursor (Prolamin).
                                                                           291 AA.
 264 GWNQQ-----GGSGGGP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 291 A
291 AA; 33661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M10092; AAA34276.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 21.6
                                                                                                                                                               Friticum aestivum (Wheat
                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 RLSEPOECSI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 NVYIPPYCTI 282
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=4565;
                                                                         GDA2 WHEAT P04722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Matches
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Q94il6 secale cere Q94ij8 triticum ae Q9sdm2 triticum ae Q93wm1 secale cere

Q941L6 Q941J8 Q9SDM2 Q93WM1

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                                                                                                           November 29, 2003, 16:53:04; Search time 56 Seconds (without alignments) 949.265 Million cell updates/sec
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                                                                                                                                                                                                                1 MAKIAAAAAALCFAALVAV..........MMCRLSEPQECSIFSGGDQY 206
                                                                                                                                                                                                                                                                                                                                        830525
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                     830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_arches:*
sp_bacteria:*
sp_fungl:*
sp_fungl:*
sp_human:*
sp_novertebrate:*
sp_mammal:*
sp_nammal:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_rodent:*
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sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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1148
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                                                                                                                                                                             Title:
Perfect score:
Sequence:
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                                                                             OM protein
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264.5         23.0         179         10         Q9MSN3         Q9mSn3 aggilops ve           260         22.6         63.1         10         Q84XN9         Q84X8         Q84X8         Q84X8         Q84X8         Q84X8         Q84X8         Q84X8         Q84X8         Q84X8         Q84X1         Q8X1         Q8XX         Q8XX<	PRELIMINARY; PRT; 206 AA.  101 (TrEMBLrel. 19, Created) 103 (TrEMBLrel. 19, Last sequence update) 104 (TrEMBLrel. 23, Last annotation update) 105 (TrEMBLrel. 23, Last sequence update) 106 (TrEMBLrel. 23, Last sequence update) 107 (Maize) 108 (Mai	100.0\$; Score 1148; DB 10; Length 206;   21 Similarity   100.0\$; Pred. No. 1.5e-105;   206;
22 25 26 27 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28	SULT 1 46V3 0946V3 01-DEC-2 01	Query Match Best Local S Matches 206  1  6  1  6  1
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14;

Gaps

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70 ----RWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKG-WWPWGRQQQ---- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 -----PPPQ-------GGGGGGGGGYYYPCSRPGEGYGYGGGGQRQMYPPC--RP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AVFLAALVAGSAAQGVLE-QSLTDAQCRGEVQEKPLLACRQILEQQLTGRAGEGAVGVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SGESTEPEOROEVOGGOYGSETGGGOOOGGGYH-----GVTVGRGGOROGOVLCHKRP
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Aegilops.
NCBI_TaxID=37682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Aegilops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 -----GITGGG----PRIGRVRLTKAREYAAGLPMMCRLSEPQECSIFSGGDQY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Endosperm;
Wan Y., Wang D., Shewry P.R., Halford N.G.;
Wan Y., Wang D., Shewry P.R., Halford N.G.;
Wan Y., Wang D., Shewry P.R., Halford N.G.;
Wan Y., Wang D., Shewry P.R., Halford N.G.;
Wan Y., Wang D., Shewry P.R., Halford N.G.;
Submit of glutenin genes from Triticum timopheevi and Aegilops
Cylindrica. ",
Submitted (APR. 2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ306974; CAC38013.1; -.
InterPro. I PR001419; Glutenin hw; 1.
PRINTS; PR00150; GLUTENIN.
                                                                                                                             Anderson O.D., Rausch C., Moullet O., Lagudah E.S.; "Characterization of a wheat D-genome BAC containing two paralogous HMW-glutenin genes: distribution of genes and retrotransposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.5%; Score 292.5; DB 10; Length 654; 36.2%; Pred. No. 1.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Indels
                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS, PR00210; GLUTENIN.
SMART; SM00499; A.A.1; 1.
SEQUENCE 226 AA; 24515 MW; 95397E83C63D50AD CRC64;
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>>54 HWW SUBUNIT 1DY.
654 MW, AC8E71075FCFD2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRAR-2003 (TrEMBLrel. 23, Last annotation update)
Glutenin HMW subunit 1Dy precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                          36.1%; Score 414; DB 10; 46.8%; Pred. No. 5.5e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.1%;
Best Local Similarity 46.8%
Matches 110; Conservative
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·22 >6
654 6
654 AA;
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Best Local Similarity
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SEQUENCE
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SIGNAL
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Q93XR5
                 SPREETTARKS
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                                    61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMP-PLEKGWWPWGRQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Endosperm;
MEDLINE=96235139; PubMed=8666249;
Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
Tanaka K., Matsuda T.;
Tonaka K., Matsuda T.;
"Cloning of rhe rice seed alpha-globulin-encoding gene: sequence
similarity of the 5'-flanking region to those of the genes encoding
wheat high molecular-weight glutenin and barley D hordein.";
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Ewkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideee, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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51.4%; Pred. No. 1.5e-35;
iive 20; Mismatches 54;
                                                                                                                                                                                                                                                                             186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 KAREYAAGLPMMCRLSEPQECSIFSGGDQY 206
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                                                                                                                                    181 YAAGLPMMCRLSEPOECSIFSGGDOY 206
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                                                                                                           YAAGLPMMCRLSEPQECSIFSGGDQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001612; AAI.
InterPro, IPR001419; Glucenin.
Pfam; PF00234; tryp, alpha amyl; 1.
PRINTS; PR00210; GLÜTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 170:223-226(1996).
EMBL; D50643; BAA09308.1; -.
Gramene; P93414; -.
                                                                                                                                                                                                                                                                                                                    01-MAX-1997 (TEMBLEEL 03, 01-MAX-1997 (TEMBLEEL 03, 01-MAR-2003 (TEMBLEEL 23, 26 kba globulin.
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Matches 108, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                                                        121
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                 121
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QBLKV8;
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P93414
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QBLKV8
ID QBLK
DT QBLK
DT 01-O
DT 01-O
DT 01-M
DE Seed
GN GLO-OS Aegi
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Triticum aestivum (Wheat).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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STRANIE-CV. Cheyenne; TISSUB=Endosperm;
Halford N.G.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                          624 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMW glutenin subunit 1By9 precursor GLU-1BY9.
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                                                           243 goldgegoldgergigge 260
                    168 PRIGR-VRLTKAREYAAG 184
                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=37682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4565
                                                                                                                                                                                                                                                                                      HMW-glutenin.
GLU-DTY.
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01-MAR-2003
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QBLKV7;
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Q8LKV7
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                                                                                                                                                        52 ----AGRLPWSTGLQMRCCQQLRDVSAKCRSVAVSQVTRQYEQTVVPPKGRSFYPGETT 106
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                                                                                                                              61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP---- 115
                                                                                                                                                                                                                   107 PLQQLQQGIFWGTSSQTVQGYYPSVTSPRQGSYYPGQASPQQPGQGQQPGKWQEPGQGQQ 166
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                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Bustos A., Jouve N., "Characterization and analysis of new subunits-like wheat HMW-glutenin "Characterization and analysis of secale."; encoded by Glu-1R gene of Secale cerale."; submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                         MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGG
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                                                                                  1 MAKRLVLFAAVV--IALVALTTABGEASRO----LOCERELOBSSLEACROVVDOOL---
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Gaps
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65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gueros A., Rubio P., Jouve N.;
"Characterization of two gene subunits on the 1R chromosome orthologs of each of the Glu-1 genes of hexaploid wheat.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
InterPro: IPR001419; GLU-Enin.
Pfam; PR03157; Glutenin.
PRINTS; PR00210; GLUTENIN.
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51; Indels
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720 HWW GLUTENIN SUBJUA.
77372 WW; 3385D2004B7D3B18 CRC64;
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                                                                                                                                                                                                                                                                                                         134 YYYPCS--RPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) High molecular weight glutenin subunit y precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 AA
25; Mismatches
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es 85; Conservative
80; Conservative
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Best Local S:
Matches 85
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107 PLQQLQQGIFWGTSSQTVQGYYPSVTSPRQGSYYPGQASPQQPGQGQQPGKWQEPGQGQQ 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Gaps
                                                                                              Aegilops tauschii (Aegilops squarrosa).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Aegilops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 624;
                                                                                                                                                                                                                                                                                                                                          Anderson O.D., Rausch C., Moullet O., Lagudah E.S.; "Characterization of a wheat D-genome BAC containing two para HMW-glutenin genes: distribution of genes and retrotransposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------RQ------RG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AF497474; AAM77581.1; -... InterPro; IPR00149; Glutenin. Pfan; PF03157; Glutenin hmw; 3. PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 AA; 67104 MW; 9EA4B0C0B41CF829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 YYYPCS--RPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 WYYPTSLQQPGGGGGGGG--QQGYYPTSLQQPGQQGQGGG 205
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.1%; Score 288.5; DB 10; Best Local Similarity 36.2%; Pred. No. 4.2e-20; Matches 80; Conservative 24; Mismatches 52;
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75

61

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59 QQL------VGQLPWSTGLQMQCCQQLRDVSPECRPVALSQVVRQYEQQTEVPSKGGS 110
                                                                                                                     .------ 117
                                                                                                                                                     122 QTVQGYYPSVTSPQQGSYYPGQASQQPGQGQHPGKWQELGQGQQGYYPTSLQQSGQGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 ROLIGGGGGGGGGGGGGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE----- 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGVGPFRWGTGL
                                                                 -----AGRLPWSTGL
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96204516; PubMed=8628236; MEDLINE=96204516; PubMed=8628236; Sorensen M.B., Muller M., Skerritt J., Simpson D.; Sorensen M.B., Muller M., Skerritt J., Simpson D.; Sorensen M.B., Muller M., Skerritt J., Simpson D.; Sorensen M.B., Muller M., Skerritt J., Simpson D.; Sorensen M.B., Muller M., Sorensen M.B., Mol. Genet. 250:750-760(1996).

Mol. Gene. Genet. 250:750-760(1996).

InterPro; IPR0013612; AAI.

InterPro; IPR0013612; AAI.

Fran, PR00151; Glutenin.

Pram, PR03157; Glutenin.

PRNNTS; PR00210; GLUTENIN.

SMART; SM00499; AAI: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 24.6%; Score 282.5; DB 10; Length Local Similarity 36.2%; Pred. No. 1.2e-19; nes 79; Conservative 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                             135 -YYPCS--RPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                            475 475
475 AA; 50786 MW; 608B05E8E0F381B3 CRC64;
                                                                 14 ALVALTAAEGEASRQ----LQCERELQESSLEACRQVVDQQL-
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Last sequence update)
Last annotation update)
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                                                                                                                     76 RMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP-
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare (Barley).
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SEQUENCE
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Best Local S:
Matches 79,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 MRCCQQLRDVSAKCRPVAVSQVVRQYEQTVVPPKGGSFYPGETTPLQQLQQVIFWGTSSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TVQGYYPSVSSPQQGPYYPGQASPQQPGQQQPGKWQELGQGQQGYYPTSLHQSGQGQQG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------GQRQMYP--PCRPG---TTGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 YYPSSLQQPGQQQGQQQQQQYYPTSLQQPGQQQQIGQGQQGYYPTSPQHPGQRQQPGQG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LVALTAABGEASRQ----LQCERBLQESSLEACRQVVDQQL-----AGRLPWSTGLQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGFRWGTGLR 76
                                       STRAIN=CV. Cheyenne; TISSUE=Endosperm;
Halford N.G., Forde J., Anderson O.D., Greene F.C., Shewry P.R.;
"The nucleotide and deduced amino acide sequences of an HWW glutenin
subunit gane from chromosome 1B of bread wheat (triticum aestivum L.)
and comparison with those of genes from chromosomes 1A and 1D.";
Theor. Appl. Genet. 75:117-126 (1987).
EmBL; X61026; CAA43361.1; -.
InterPro; IPR001419; Glutenin.
Pfam; PF03157; Glutenin.
Pfam; PF03157; Glutenin.
Pfam; PR001610; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aegilops speltoides (Goat grass).
Eukaryota, Varidiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Aegilops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Bustos A., Corredor M., Jouve N.S.; "Characterization of HMW glutenins in diploid species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                      HMW GLUTENIN SUBUNIT 1BY9,
E8BC745940710FF8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%; Score 287; DB 10; 32.9%; Pred. No. 6.8e-20; tive 24; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      704 AA
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InterPro, IPR01419; Glutenin.
Pfam; PF03157; Glutenin hmw; 4.
PRINTS; PR00210; GLUTENIN.
SEQUENCE 704 AA, 75932 MW; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 QQİĞQGQQLGQGRQIGQĞ 260
                                                                                                                                                                                                                                                                                                                                                                                                                                75702 MW;
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22
705 AA;
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Best Local Similarity
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SIGNAL
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QBLKIB;
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59 QQL-----VGQLPWSTGLQMQCCQQLRDVSPECRPVALSQVVRQYEQQTEVPSKGGS 110
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                                                                                                                                                                                                                                                                                                    55 RQLTGGGGGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEE----- 104
                                                                                                                                                                                                                                                                                                                                                                                               111 FYPGGTAPPLQQGGWWGTSVKWYYPDQTSSQQSWQGQQGYHQSVTSSQQPGQGQQGSYPG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ----AGRIPWSTGLQMRCCQQLRDVSAKCRSVAVSQVARQYEQTVVPPKGGSFYPGETT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 PLQQLQQGIFWGTSSQTVQGYYPSVTSPRQGSYYPGQASPQQPGQQQPGKWQEPGQGQQ 166
                                                                                                                                                                                                                                                           1 MAKIAAAAAALCFAALVAVAVCQGEVE-----RQRLRDLQCWQEVQESPLDACRQVLD
                                                                                                                                                                                                                                                                                                                                                                   105 ----AMPPLEK-GWW-------PWGRQQ-----QPPPQGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan S., Guo A., Luo D., Zhao H., Feng X.; "Partial seqence of wheat HMW-GS(Dy type) gene from cultivar 'Xiaoyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum (Wheat).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.2%; Score 277.5; DB 10; Length 196; 36.7%; Pred. No. 1.4e-19; tive 22; Mismatches 44; Indels 65;
                                                                                                                                                                          DB 10; Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ308967; CAC84118.1; -- NON_TER 196 196
                                                                                                          28 POTENTIAL.
707 D HORDEIN.
75108 MW; EBB873AF035D5789 CRC64;
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SEQUENCE 196 AA; 21587 MW; 4B48BE38F40A4D07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               134 YYYPCSRPGEGYGYGQGGQRQ--MYP----PCRPGTTGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 STFP-QOPGQGQ---QPGQRQPWSYPSATFPQQPGQGQG 205
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                                                                                                                                                                       Query Match
24.5%; Score 281.5; DB 10
Best Local Similarity 36.1%; Pred. No. 2.4e-19;
Matches 79; Conservative 22; Mismatches 51
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                                         Pfam; PF03157; Glutenin hmw; 1.
PRINTS; PR00210; GLUTENIN.
SMART; SM00499; AAI; 1.
                nterPro; IPR003612; AAI.
interPro; IPR001419; Glutenin.
 EMBL; D82941; BAA11642.1; -.
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Best Local Similarity 36.74
Matches 76; Conservative
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29 7
707 AA;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGRLPWSTGLQMRCCQQLRDVSAKCRSVAISQVARQYEQTVVPPKGGSFYPGETT 106
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                                                                                                                                                                                                                    Mackie A.M., Sharp P.J., Lagudah E.S.;
"The nucleotide and derived amino acid sequence of a HMW glutenin gene from triticum tauschii and comparison with those from the D genome of bread wheat.";
J. Cereal Sci. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKIAAAAAALCFAALVAVAVCQGEVERQRIRDIQCWQEVQESPLDACRQVLDRQLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mackle A.M., Lagudah B.S., Sharp P.J., Laflandra D.;
"Molecular and blochemical characterisation of HWW glutenin subunits
from T. tauschii and the D genome of hexaploid wheat.";
T. Cereal Sci. 0:0-0(1996).
EMBL; U39229; AAC15244.1;
                                                                                                                         Bukaryota, Viridiplantae, Stréptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Aegilops.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 24.6%; Score 282; DB 10; Length 648; Local Similarity 37.1%; Pred. No. 1.9e-19; les 79; Conservative 22; Mismatches 46; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Haruna Nijo; TISSUE-Endosperm;
Hirota N., Kuroda H., Ito K.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69567 MW; ESD71332E520DF5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 WYYPTSLOOPGOGOGIGK-GOOGYYPTSLOOPG 198
648 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               707 AA
                                                                           High molecular weight glutenin subunit
                                                                                                          Aegilops tauschii (Aegilops squarrosa)
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PRT:
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InterPro; IPR001419; Glutenin.
Pfam; PF03157; Glutenin.hmw; 1.
PRINTS; PR00210; GLUTENIN.
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                             (TrEMBLrel. 01,
                                            01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
PRELIMINARY:
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                                                                                                                                                                          NCBI_TaxID=37682;
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                               01-NOV-1996
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Matches
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RESULT 13 Q8S3V7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GHYPASQQQPGQQQGHYPASLQQPGQGQQGHYPASLQQPGQGQQTEQPGQMQQPGQGQQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ÓTVQGYYPSVTSPQÓGSYYPGQASPQQPGQQQQGKWQEPGQGQQGYYPTSQQQPGQGQ 181
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Secale.
                                                    of rye
                                                                                                                                                                                                                                                                                                                  98;
         GERAIN-CV. Imperial;

de Bustos A., Rubio P., Jouve N.;

characterization of two gene subunits on the 1R chromosome corthologs of each of the Glu-1 genes of hexaploid wheat.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ314781; CAC40682.1;

InterPro; IPR001419; Glutenin.

PÉAM; PR03157; Glutenin hww; 1.

PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                         Ouery Match 24.0%; Score 275; DB 10; Length 713; Best Local Similarity 32.1%; Pred. No. 1.1e-18; Matches 78; Conservative 21; Mismatches 46; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wheat.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Bustos A., Jouve N.;
"Characterization and analysis of new subunits-like whea
encoded by Glu-1R gene of Secale cereale.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Bustos A., Rubio P., Jouve N.; "Characterization of two gene subunits on the 1R chromos orthologs of each of the Glu-1 genes of hexaploid wheat. Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    713 HMM GLUTENAM 76274 MW; 49EEB182BBC19C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             76 RMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWP---
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01-DEC-2001 (TrEMBLrel, 19, Last seq
01-MAR-2003 (TrEMBLrel, 23, Last ann
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InterPro; IPR001419; Glutenin.
Pfam; PF03157; Glutenin hmw; 1.
PRINTS; PR00210; GLUTENIN.
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713 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YYPCS--RD-----ROEPPQGGGGGGGGG------YYPCS--RPGEGYG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 QTVQGYYPSVTSPRQGSYYPGQASPQQPGQGQQPGKWQEPRQGQQGYYPTSLQQPVQGQQ 181
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnollophyta, Lilliopsida, Poales; Poaceae, Pooldeae;
Triticeae, Aegilops.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Secale.
NCBI_TaxID=4550;
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                                                                                                                                                                                                                                                                                                                                                                                      Liu Z., Yan Z., Wan Y., Liu K., Zheng Y., Wang D.;
"Analysis of HMW glutenin subunits and their coding sequences
diploid Aegilops species.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF476962; AAL82616.1; -.
InterPro; IPRO01419; Glutenin.
Pfam; PF03157; Glutenin hmw; 1.
SEQUENCE 655 AA; 70458 MW; 20F0A70E4D54FF2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%; Score 276.5; DB 10; Length 655; 36.3%; Pred. No. 6.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
High molecular weight glutenin subunit y precursor.
                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                655 AA
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YYYPCS--RPGEGYGYGQGGQRQMYPP 158
                   167 WYYPTSLQQPGQGQGIGKG--KQGYYP 191
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                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                        HMW glutenin subunit.
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4491;
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01-OCT-2002
134
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RESULT 14
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AC 0941K
DT 01-DE DT

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		99; Сарв	RWGTGL	VGRLPWSTGL 61	-WGRQQ	FWGTSS	135	PGQGQQ	GR 172	: GQ 229	
			GVGPF	VGRL		PLOOGI		TSLOO	GGPRI	0910090s	
RC64;	23.3%; Score 267.5; DB 10; Length 737; 31.8%; Pred. No. 6e-18;	Indels	16 ALVAVAVCQGEVERQRIRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGGFRWGTGL 75	or	76 RMRCCQQLQDVSRECRCAAIRSMVRGYEE-AMPPLEKGWWPWGRQQ 120	62 HMRCCQQLRDVSAKCRHVAVSQVARQYEQTTVPPKGGSFYPSETTPLQQLQQGIFWGTSS 121	GGGGGXX	122 ÓTVQGYYPSVTSPQQSYYPGRASPQQPGQGQQPGKWQEPGQGQQGYYPTSLQQPGQGQQ 181	YPCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172	182 EHYPASQQQPGQQGHYPASLQQPGQGQTGQPGQIQQPGQGQQIGQ 229	
0F06 C	OB 10;	44;	ROVLDR	)ÖQAAÖ	LEKGWW	KGGSFY	)	3KWQEP(	SOROMY	30100-	
979829	7.5; . 6e-1	cches	SPLDAC	SSLEAC	S-AMPP	TTVPP	:	SOGOOP	rGYGOG	2QTGQP(	
25E1BF	ore 26 ed. No	Мівша	WOEVOE	EHELQE	MVRGYE	VARQYE		ASPOOP	RPGEGY	00PG0G	
W.	Son	18;	DIOC	-07 	AIRS	AVSQ		YPGR	PCS-	PASL	
79406 MW; 25E1BF9798290F06 CRC64;	23.3%;	tive	SVERORLE	14 ALVALTAAEGEASGQLQCEHELQESSLEACRQVVDQQL	SRECRC	RCCQQLRDVSAKCRHVĀVSQVARQYEQTTVPPKGGSFYP	121 QPPPQGG	SPOOGSY	7	кнодоров	
737 AA;	arity	onserva	VAVCOGE	LTAAEGE	COOLODY	COOLRDV		GYYPSVT		ASQQQPG	
	Simi]		ALV	ALV?	RMR	HMR	è-	OTV	į	EHYI	
SEQUENCE	Query Match 23.3%; Score 267.5; DB Best Local Similarity 31.8%; Pred. No. 6e-18;	Matches 75; Conservative 18; Mismatches 44; Indels	16	14	16	62	121	122	136	182	
SQ	One	Mat	ò	В	ò	g G	ò	QQ	È	g	

Search completed: November 29, 2003, 17:06:33 Job time : 61 secs

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Sequence

30613, 21588, 22121, 19857,

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Run on:

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Title: Perfect

Searched:

Database

Result М В

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24 QGEVERQRLRDLQC---WQEVQESPLDACRQVLDRQLTGGGGGGGGGGGFRWGTGLRMRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: USDA, AGRICULTURAL RESEARCH SERVICE, PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANDERSON, OLIN D
TITLE OF INVENTION: ALTERING DOUGH VISCOELASTICITY WITH
MODIFIED GLUTENINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALMANDE FORCE

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PILING DATA:

APPLICATION NUMBER: US/08/706,391B

FILING DATE: 30-A49-1996

CLASSIFICATION: CURKNOWN-

ATTORNEY/AGENT INFORMATION:

NAME: CONNOR, MARGARET A

REGISTRATION NUMBER: 0235.95/USDA96-001

TELEPHONE: (510) 559-6067

TELEPHONE: (510) 559-5777

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
          US-09-010-928B-4

US-09-52-991A-29972

US-09-252-991A-292864

US-09-252-991A-29467

US-09-252-991A-29467

US-09-252-991A-26804

US-09-252-991A-16821

US-08-8782-177-2

US-08-782-177-1

US-08-252-991A-30613

US-09-252-991A-30613

US-09-252-991A-30613

US-09-252-991A-22128

US-09-252-991A-22128
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US-08-937-067-14
US-09-010-928B-28
US-09-010-928B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.4%; Score 130.5; DB 3
Best Local Similarity 27.2%; Pred. No. 1.6e-05;
Matches 55; Conservative 21; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EGEASEQ----LQCDRELQELQERELKACQQVMD----
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-706-3918-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 800 BUCHANAN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08706391B
Patent No. 6174725
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94710
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ALBANY
STATE: CALIFORNIA
COUNTRY: USA
RESULT 1
US-08-706-391B-7
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17915, A
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28453, A
30202, A
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24358, A
59, Appl
32227, A
2, Appli
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2, Appli
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                                                                                               November 29, 2003, 17:04:04; Search time 22 Seconds (without alignments) 396.183 Million cell updates/sec
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1 MAKIAAAAAALCFAALVAV......MMCRLSEPQECSIFSGGDQY
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-252-91A-2549

US-07-918-023-2

US-09-252-991A-17887

US-09-252-991A-1987

US-09-252-991A-1987

US-09-252-991A-19574

US-09-252-991A-1915

US-09-252-991A-1915

US-09-252-991A-1915

US-08-252-991A-24513

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US-09-252-991A-24513

US-09-252-991A-24513

US-09-252-991A-24513

US-09-252-991A-245569

US-09-252-991A-25270
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-09-252-991A-22270
-09-252-991A-31834
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                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                      - protein search,
                          Copyright
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114.5
109.5
103
101.5
100.5
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94.5
54.5
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Length 157;

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APPLICANT: Zimmermann, Thomas
APPLICANT: Zimmermann, Thomas
APPLICANT: Robins, Karen
APPLICANT: Birch, Olwen
APPLICANT: Bohlen, Elisabeth
APPLICANT: Bohlen, Elisabeth
APPLICANT: Bohlen, Elisabeth
TITLE OF INVENTION: GENETIC ENGINEERING PROCESS FOR THE
TITLE OF INVENTION: BY MICRORGANISMS
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Fisher, Christen & Sabol
STREET: 2000 M Street, N.W., Suite 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGGG----VGPFR-WGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 GAGGGRCRRAEPWRIQGIGRRAAPAA----VARACRCLRPRORIACVARTAPGGERRAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 WGRQQQPPPQGGGGGGGGYYYPCSRPGEGYG-YGQGGQRQMYPPCRPGTTGGGPRIGRVR
                                                                                                                                                                                                                                                                                              Length 410;
                                                                                                                                                                                                                                                                                        Query Match
10.0%; Score 114.5; DB 4;
Best Local Similarity 36.2%; Pred. No. 0.0018;
Matches 47; Conservative 10; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,023
FILING DATE: 19220724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19920724
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 2247/91
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07918023
Patent No. 5427934
                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,083
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TELEPHONE: (202) 659-2000
TELEFAX: (202) 659-2015
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25812
LENGTH: 410
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TELERAX: (202) 659-2015
TELEX: 248748
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 426 amino acids TYPE: AMINO ACID
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILING DATE: 107196.136
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/24,788
                                                                                                                                                                                        90 KRYYPSVTCPQ-----QVSYYPGQASPQRSSSSYHVSVEHQAASLKVAKAQQLA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VGPFRWG------TGLRM-----TGLRM-----RCCQQLQDVSRECRCAAIRSMVRGY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 EEAMPPLEKGWWP-----GQGGY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 YYPCSRPGEGYGYG-----QGGQRQMYPPC----RP-GTTGGGPRIGRVRLTKARE 180
                                    --- GGGGGGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 SGPGRAGRRSIPPAPRRGPRLARPSRGRGRTRAPGRCCSGWW--STGSPMAPVRSACRGT 86
                                                                           32 QQLRDISPECHPVVVSPVAGQYEQQIVVPP--KGGTFYPGGTTPPQQLQQRIFWGIPALL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- AGPGRGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.0%; Score 115; DB 4; Length 308; Best Local Similarity 25.0%; Pred. No. 0.0012; Matches 64; Conservative 13; Mismatches 69; Indels 110;
                                    QQLQDVSRECRCAAIRSMVRGYEE--AMPPLEKGWWPWGRQQQPPPQ---
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US-09-252-991A-27249
; Sequence 27249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25812, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                   183 AGLPMMCRLSEPQECSIFSGGD 204
                                                                                                                                                                                                                                                                                                                             ----EĞĞD 151
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US-09-252-991A-27249
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US-09-252-991A-25812
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Sequence 19574, Application US/09252991A

Sequence 19574, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

PAPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENTH: 863
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLRIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                      61 GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPL-----EKG 112
                                                                                                                                                                                                                                                                                                     -- 151
                                                                                                                                                                                                                                                                                                                                                                                                                      232 ----GAÓGARPGÓPGRAGGOGRTHPGARGGDAGLARRGEAGLAGHGYGAGATAGPRLGAG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 GGGGGGGGGGGGGTGLRMRCCOOLODVSRECRCAAIRSMVRGYEEAMPPLEKGWWPW-- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 GRQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGRVRLT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 GR-ADPPYRPGHRORGACPAPTGRPGOG----RGERR---PVVRRTPGAGPRL---- 247
                                                                                                                                                                       9
                                                                                                                                                                       2 AKIAAAAAAALCFAALVAVAVCQGE-VERQRIRDLQCWQEVQESPLDACRQVLDRQLTGG
                                                                                                                      76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 -------OROMYPPCRPGTTGGG--PRIGRVRLTKAREYAAGLP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 LAAARQGLDGIALNLDRRTRPTCRPGSFGADVEPAAGLADDTEARVAVRGDP 339
                                                                     9.0%; Score 103; DB 4; Length 476; 25.9%; Pred. No. 0.03; tive 17; Mismatches 79; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 101.5; DB 4;
29.5%; Pred. No. 0.082;
trive 14; Mismatches 48;
                                                                                                                                                                                                                     137 ASRSADAARAVPAIAGASAAEROGRPAGDORLR-----
                                                                                                                                                                                                                                                                                                                                                                     113 WWPWGRQQQPPPQGGGGGGGGYYYPCSRPGE-
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                     Query Match
Best Local Similarity 25.9%
Matches 60; Conservative
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Best Local Similarity 29.5%
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 --RRPAGGVPRL 257
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US-09-252-991A-28410
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          ; OKGANISM: PBEUGO
US-09-252-991A-17887
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17887
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 IGRQRHHGAQAHLGQGEPPRLRTGRVPGPHR-------PDGAQCCRC--RSH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 ARGHRRGGPAGPYGQPVQRARLSGHDDARILRPAPGHGPAMGTGRRGCPLPPGGGAGPGG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 ------GAAPGGQRAGGPLSRCHPG--GGGLAGAVRGGDRRGARRHVPCTARGL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GPPRWGTGLRMRCCQOLQDVSRECRCAAIRSM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 109.5; DB.1; Length 426; 22.8%; Pred. No. 0.006; tive 16; Mismatches 70; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 QGEVERQRLRDLQCWQEVQESPLD--ACRQVLDRQLTGGGGGGGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 -PRIGRVRLTKAREYAAGLPMMCR----LSEPQECSIFSGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 WPRARRVDRPGAGPVRHRLPAAAAAPRGLHGPGACTLRAGG 373
                                                2: FROM 1 TO 426
                                                                                                                                             2: FROM 1 TO 426
                                                                                                                                                                                                                                               2: FROM 1 TO 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17887, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
DOCUMENT NUMBER: RO 92-01033
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
DOCUMENT NUMBER: SU UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                             FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                  FILING DATE: 23-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                          DOCUMENT NUMBER: JP 198717/92
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
DOCUMENT NUMBER: CS PV2323-92
                                                                                                                                                       PUBLICATION INFORMATION:
nOCUMENT NUMBER: PL P 295408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HU P9202439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.8%
Matches 64; Conservative
                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
DOCUMENT NUMBER: HU PO
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-252-991A-17887
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NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOMAL CHROMOSOMAL TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 VRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGYYYPCSRPGEGYGYGGGGQRQMYPP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 100; DB 2; Length 656;
18.4%; Pred. No. 0.084;
ve 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBA:
APPLICATION NUMBE: DCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: AEDIT 1.0 DOS text editor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Weiser & Associates
230 South Fifteenth Street
                                                                                                                             Sequence 2, Application US/08343443B Patent No. 5968734
                                                                                                                                                                                                                                                                                                                                    Ploougastel, Beatrice
Thomas, Gilles
Zucman, Jessica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                                                                                                       Aurias, Alain
Delattre, Olivier
Desmaze, Chantal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               Melot, Thomas
Peter, Martine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 CRPGTTGGGPRIG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 RGPRGSRGNPSGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 38.4
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHROTITLE OF INVENTION: THATLE OF INVENTION: TRATITLE OF INVENTION: TRANIUMBER OF SEQUENCES: 123 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 230 COTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19102
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                                                                             RESULT 9
US-08-343-443B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-343-443B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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US-05-25-91A-10648

US-05-25-91A-10648

Sequence 30648, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCSA 136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION UNMBER: US 60/094,190

PRIOR APPLICATION UNMBER: US 60/094,190

PRIOR APPLICATION UNMBER: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 RMRCCOOLODVSR-----ECRCAAIRSMVRGYEEAMPPLEKGWWPWGRQ----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 DRRDRQLPHRGGPRPGQAGQAGRWPGAPHQRPGRRRQWHPLHRQRGLRHRHRGLGHAGRR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ACRQVLDRQLTGGGGGGG-----VGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GEGY-----GYGQGGQRQMYPPCRPGTTGGGPR--IGRVR---LTKAREYAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 GQRDRPRADRAQ------PAAACR----RHARGNPRGVLLGEPAGPRPVGEHPWHPGL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EGYGYGQGGQR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GYEEAMPP--LEKGWWPWGRQQQPPPQGG-----GGGQGGYYYPC----SRP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 -----WPPGLLEPG--PGGRATHPDPAPGHRTAGGNRAGDPRGGYRYGARPGHRHRRHRP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GPGQRTAAVDGDCGGPRGRGRGAGRAQSPAVAPGERRGAPQPLVLRSRWPTLPDDRRQSA 184
                                                                                                                                                                                                                                                                                                                                                                                                                    ----GGGGGVGPFRWGTGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AORPARHRVAAGGGDGQAAQLPAYLAGAHRAARG--QRAVRRLDRPSAQRRAGGLHT---
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 QMYPP--CRPGTTGGGPRIGRVRLTKAREYAAGLPMMCRLSEPQECSIFSGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 ORAPPGRLKPGDOGOHWRAAHRRLVQSRGRAAG-------QAFAGG 364
                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                               Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 100; DB 4; Length 209; 27.1%; Pred. No. 0.023; tive 12; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                            8.8%; Score 100.5; DB 4;
26.7%; Pred. No. 0.06;
iive 12; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                 25 GEVERORIRDLQCWQEVQESPLDACRQVLDRQLTGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ----QQPP----PQGGGGGGGYY--YPCSRPG-
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28410
LENGTH: 535
                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26./*
Best Local Similarity 26./*
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Best Local Similarity 27.13
Matches 52; Conservative
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                                                                                                                                                                                                                                                            US-09-252-991A-28410
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LENGTH: 209
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99 VRG-YEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYP 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 QEVQESPLDACRQVLDRQLTGGGGGGGGGGFFRWGTGLRMRCCQQLQDVSRECRCAAIRSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 124;
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MIYAZAKI, TOSHIYUKI
APPLICANT: MORIMOTO, TOSHIYUKI
APPLICANT: MORAYAMA, RYUJI
APPLICANT: MATSUBARA, HIROSHI
APPLICANT: MATSUBARA, HIROSHI
TITLE OF INVENTION: AMYLASE INHIBITORS
INWBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON: SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER KEALABLE FORM:
MEDIUM TYPE: FIDDPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,846
FILING DATE: 24-MAR-1994
CLASSIFICATION NUMBER: US/08/216,846
FILING DATE: 29-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 91881/1993
FILING DATE: 29-MAR-1993
PRIOR APPLICATION NUMBER: UP 148423/1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5444046man F.
REFERENCE/POCKET NUMBER: 1327-029-0X
TELECOMMUNICATION NUMBER: 1327-029-0X
TELECOMMUNICATION NUMBER: 1327-029-0X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HGAQEGQAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.018;
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Pred. No. 0.018
8; Mismatches
                                                                                                                      US-08-216-846-2; Sequence 2, Application US/08216846; Patent No. 5444046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 413-3000
TELEFAX: (703) 413-3220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHÂRATERISTICS:
LENGTH: 124 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |:|
61 LDSMYKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match . 8.6%;
Best Local Similarity 27.6%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-216-846-2
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US-08-782-177-3
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Patent No. 6551795
GENERAL INFORMATION:
FAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
Sequence 4, Application US/09214564A

Patent No. 6150515

GENERAL INFORMATION:
THEORY Sharp, Phillip A.
APPLICANT: Sharp, Phillip A.
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
TITLE OF INVENTION: Blongation By HIV-1 TAT
TITLE OF INVENTION: Mo656/7042
CURRENT APPLICATION NUMBER: US/09/214,564A
CURRENT FILING DATE: 1999-08-18
PRIOR PRING DATE: 1996-07-03
PRIOR PLING DATE: 1996-12-13
PRIOR PPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 VRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGYYYYPCSRPGEGYGYGQGGQRQMYPP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 CRIVARRRATGREGASSGGAAASGSPRATAPGIRRR----SVPARCGCVA----AGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 EEAMPPLEKGWWPWGRQQQPP----PQGGGGGGYYYPCSRPGEGYG--YGQGGQRQMY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 MRG---GLPPRE----GRGMPPPLRGGPGGPGGPMGRMG-----GRGGDRGGFPP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 WRSARPLA---WPRGRRGSAPVRRGPRRRSGGSAPGTAPRRRGTGRAIRHDRGSHRAVC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 CROVLDROLTG-----GGGGGGGGGGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.7%; Score 100; DB 3; Length 656; Best Local Similarity 38.4%; Pred. No. 0.084; Matches 28; Conservative 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
8.6%; Score 99; DB 4; Length 238;
Best Local Similarity 28.1%; Pred. No. 0.033;
Matches 39; Conservative 8; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 PP-----CRPGTTG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 CRPGTTGGGPRIG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 RGPRGSRĠNPSGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-252-991A-17915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-214-564A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 656
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GENERAL INCORNATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 ACRPRPGATAGDRRIRGATADQPGDPGGRRQRPSGGGHYRRIRTAQRSRPAGGRIRLCRL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 ----QLQDVSRECR---CAAIRSMVRGYEEAM--PPLEKGWWPWGRQQQPPPQGGGGGGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 SGOPÓLRFAAGOARRAWCGLSRRVAPGIPGALRIPPGGRGEOP-GSAAQPSAASGGTGOP 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 G-RHPLRRKPPGDTAGAYPGEPSAAPRRVPARRGRRACAGRGATRQPAAVCAEQRGAGGP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GLVEHÖRAGLRRLARRHVLRGGÖRHPLPALHRAAGR---GGAGVHPRQAAEGTGLHPVRR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 ARGHRVGDPGAGDHRCAHPAGRPANESHAQGLRHHLRQRRQRRRGDGRPGRTARRYRPAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GYEEAMPP-LEKGWWPWGRQQQPPPQGG--GGGQGGYY--YPCSRPGEGYGYGQGGRQM 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 GTGNPLPQWRDRGVWRLRRGAQPPGQGRRLAGQQAGALRRLPGGRPGD-----PRRLL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YGQGGQRQMYPPCRPGTTGGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 GEVEROR--LRDL---QCWQEVQESPLDACROVLDRQLTGGGG------GGGVGPFRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ACR----QVLDRQLTG-----GG-----GGGGVGPFRWG----TGLRMRCCQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.6%; Score 98.5; DB 4; Length 639; Best Local Similarity 26.7%; Pred. No. 0.11; Matches 58; Conservative 17; Mismatches 73; Indels 6
                                                                                                                                                                                                                                                                                                                                                               Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 YPPCRPGTTGGGPRIGRV--RLTKAREYAAGLPMMCR 190
                                                                                                                                                                                                                                                                                                                                     ..; DB 4;
                                                                                                                                                                                                                                                                                                                                                            Query Match

8.6%; Score 98.5; DB 4; 1
Best Local Similarity 27.7%; Pred. No. 0.1;
Matches 53; Conservative 12; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 GTGLRM------RCCQQLQDVSRECRCAAIRSMVR-
  CURRENT APPLICATION NUMBER: US/09/252,991A
                         CURRENT FILING DATE: 1999-02-18
PRIOR PEDICATTON NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24513
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28453, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GYYYPCSR--PGEGYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 RIGRVRLTKAR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 GSGRWRTGACR 521
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 VRG-YEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 QEVQESPLDACRQVLDRQLTGGGGGGGGGFFRWGTGLRMRCCQQLQDVSRECRCAAIRSM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 QAFQVPALPACRPLLRLQCNGSQVPEAV-----LR-DCCQQLAHISEWCRCGALYSM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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Pred. No. 0.018;
8; Mismatches 38; Indels 6
                                                                                                      APPLICANT: MORIMOTO, TOSHHHISA
APPLICANT: MURAYMA, RYUJI
APPLICANT: TAKASE, SACHINO
APPLICANT: GADA, TOSHHNAO
TITLE OF INVENTION: AGENTS FOR INHIBITING ACCUMULATION OF
TITLE OF INVENTION: VISCERAL FAT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                      F: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LDSMYKE-----HGAQEGQAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRILIGATION NUMBER: US/08/782,177
FILING DATE: 14-JAN-1997
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 PCRPGTTGGGPRIGR -- VRLTKAREYAAGLPMMCRL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TGAFPRCRREVVKLT-----AASITAVCRL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1327-055-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 23445/1996
FILING DATE: 18-DAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
Sequence 3, Application US/08782177
Patent No. 5789380
GENERAL INFORMATION:
                                                                                  MIYAZAKI, TOSHIYUKI
MORIMOTO, TOSHIHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.6%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 124 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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US-09-252-991A-24513
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
ADDRESSEE:
STREET: 175
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Search completed: November 29, 2003, 17:07:34 Job time : 25 secs

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Sequence

Sequence 37, Appl Sequence 57, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 7, Appli Sequence 10, Appli Sequence 10, Appli Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2268, Appl Sequence 2268, Appl Sequence 2268, Appl

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Sequence 34, Appl
Sequence 324, App
Sequence 438, App
Sequence 1664, Ap
Sequence 12824, A
Sequence 80, Appl
Sequence 80, Appl
Sequence 116, Appl
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Sequence 337, App
Sequence 337, App
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAKIAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQ---VLDRQL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 WGRQQQPPPQGGGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYPPC-----RPGTTGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.2%; Score 117; DB 12; Length 169;
Best Local Similarity 23.9%; Pred. No. 0.0097;
Matches 56; Conservative 24; Mismatches 56; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10165289A

Publication No. US20030159174A1

GENERAL INFORMATION:
APPLICANT: QIU, Xiao
APPLICANT: TRUSKA, Martin
APPLICANT: TRUSKA, Martin
APPLICANT: HU, Zhiyuan
TITLE OF INVENTION: Flax (Linum usitatissimum L.)
TITLE OF INVENTION: Seed-Specific Promoters
FILE REFERENCE: BNZ-005
CURRENT APPLICATION NUMBER: US/10/165,289A
CURRENT PILING DATE: 2002-06-06
PRIOR PILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 169
5 US-10-184-634-59

2 US-10-168-097A-36

2 US-10-153-668-334

5 US-10-153-668-438

6 US-09-925-300-1664

6 US-09-925-300-1664

105-09-864-761-43644

105-09-864-761-43644

105-09-864-761-43644

105-09-817-102A-37

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; ORGANISM: Linum usitatissimum
US-10-165-289A-4
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Sequence 2, Appli
Sequence 73, Appli
Sequence 56, Appli
Sequence 51, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 670, Appl
Sequence 1120, Appl
Sequence 1120, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                    November 29, 2003, 17:06:40 ; Search time 46 Seconds (without alignments) 825.985 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-866-557A-5
US-10-055-797-5
US-10-165-289A-2
US-09-847-102A-73
US-09-847-102A-56
US-10-285-976-53
US-10-235-976-53
US-10-233-553-23
US-10-233-553-11
US-10-233-553-11
US-10-233-553-11
US-10-156-761-11120
US-09-861-597-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673684 seqs, 184443283 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1148
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Match Length DB
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13

98; Gaps

117 106.5 106.5 105.

Result

100.5 97.5 97.5 96.5

101

33

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47 QOLQOPQ--QQQQQQPHQQQQQSSRQQPSTSSGGSRASGFQQGGQQQKSQDAEGWTAQKK 104
                                                                                                                                                                                                                                                                                                                Sequence 2. Application US/10165289A;
Publication No. US20030159174A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: QIU, Xiao
APPLICANT: TRUSKA, Martin
APPLICANT: TRUSKA, Martin
APPLICANT: TRUSKA, Martin
APPLICANT: TILE OF INVENTION: Seed Specific Promoters
FILE REFERENCE: BNZ-005
CURRENT APPLICATION NUMBER: US/10/165,289A
CURRENT APPLICATION NUMBER: 60/295823
FRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/295823
FRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FasteseQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 IRSMVRGYEEAMPPLEKGWWPWGRQQQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.5*
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-165-289A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 RCCQQLQDVSRECRCA----AIRSMVRGYEEAMPPLEKGWWPWGRQ------QQPPP--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 QRIRDLQCWQEVQESPLDACRQVLDRQLTGGGGGGGGGGVGPFRWG------TGLRM 77
                                                                                                                                                                                     Sequence 5, Application US/09866557A

Sequence 5, Application US/09866557A

Sequence 5, Application US/09866557A

SEQUENCE 5, Application US/09866557A

GENERAL INFORMATION:

APPLICANT: Hammond, S.

APPLICANT: Hammond, G.

APPLICANT: Beach, D.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE

FILE REFERENCE: GNCA-PO2-007

CURRENT PILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: 60/189,739

PRIOR APPLICATION NUMBER: 60/189,739

PRIOR APPLICATION NUMBER: 60/189,739

PRIOR PILING DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH. 1145
                                                       165 QGGHQQGRQGQEGGYQQRPSGQQQGGHQQGRQGQEGGYQQRPPGQQQGGHQQGR 218
                            168 -PRIGRVR-------LIKAREYAAGLPMMCRLSEPQECSIFSGGDQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 -----OGGGGGGGGYYY-PCSRPGEGYGYGOGGQROMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hammond et al.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
FILE REPERENCE: GRCA-P03-00-0
CURRENT APPLICATION NUMBER: US/10/055,797
CURRENT FILING DATE: 2002-01-22
PRIOR PPLICATION NUMBER: 60/189,739
PRIOR FILING DATE: PCT/US01/08435
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.3%; Score 106.5; DB 10; Length 1145; l Similarity 25.9%; Pred. No. 0.54; 45; Conservative 25; Mismatches 71; Indels 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Drosophila melanogaster
US-10-055-797-5
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Best Local Similarity
Matches 45; Conserva
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Best Local Similarity
Matches 45; Conserva
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US-10-055-797-5
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Sequence 73, Application US/09847102A

Publication No. US20030044409A1

Publication No. US20030044409A1

GENERAL INFORMATION:

APPLICANT: University of California

APPLICANT: Corr. Maripat

APPLICANT: Corr. Maripat

APPLICANT: Lorenzo, Leoni M.

APPLICANT: Rhee, Chae-Seo

APPLICANT: Lorenzo, Leoni M.

APPLICANT: Nation Sen

ITILE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

ITILE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

TURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 73

LENGTH: 277
78 RCCQQLQDVSRECRCA----AIRSMVRGYEEAMPPLEKGWWPWGRQ-----QQPPP--- 124
                                                                        105 ОСКОДУОСМТКОСООССНООСКОСОВСЯЙОСЯРРСОООССНООСКОСОЕССЯЙОЯРРСОО 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 QDYLRSCQQFLWEKVQKGGRSYYYNQGRGGQQSQHFDS----CCDDLKQLRSECTC-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SP-LDACROVL-DROLTGG-----GGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- QGEVERQRLRDLQCWQEVQE
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                                                                                                                                                                                                                              165 QGGHQQGRQGGGGYQQRPSGQQQGGHQQGRQGGGQQQRPPGQQGGHQQGR 218
                                                                                                                                                                  125 -----QGGGGGGGYYY-PCSRPGEGYGYGQGGQRQMYPPCRPGTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 105; DB 12; Length 168; 26.5%; Pred. No. 0.11; trive 21; Mismatches 45; Indels 4;
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APPLICANT: Rhee, Chae-Seo
                         Malini, Sen
Wu, Christina
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: MRI-044
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APPLICANT: Carson, Dennis A.
APPLICANT: Carson, Dennis A.
APPLICANT: Carson, Dennis A.
APPLICANT: Ree, Chae-Seo
APPLICANT: Ree, Chae-Seo
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 2200-20629.00
CURRENT PAPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARES FARSEQ for Windows Version 4.0
SEQ ID NO 56
                                                                                           Gaps 10;
                                                                                                                                                                                                                                                                 85 KFFLCSMYTPICLEDYKKPLPPCRSVCER-----AKAGCAPLMRQYGFAWPD--RMRCD 136
                                                                                                                                                                                                                                                                                                                81 QQLQDVSRECRC----AAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYY 135
                                                                                                                                                                                                                                                                                                                                                               137 RLPEQGNPDTLCMDYNRTDLTTAAPSPPRRLPPPPPG-----EQPPSGSGHGRP--- 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 QOLQDVSRECRC----AAIRSMVRGYEEAMPPLEKGWWPWGRQQQPPPQGGGGGGGGYY 135
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                                                                                                                                                                  42 Q-----FRWGTGLEMRCC 80
                                                                                                                                    ---EVER-QRLRDLQCWQEV 41
                                                                                                                                                                                                                           42 Q------FRWGTGLRACROVLDRQLTGGGGGGGGGGGG-----FRWGTGLRARCC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AAAAAAALCFAALVAVAVCQG-----------EVER-QRLRDLQCWQEV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Gaps
                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.1%; Score 105; DB 11; Length 694;
23.7%; Pred. No. 0.44;
tive 22; Mismatches 72; Indels 7
                                               Length 277;
                                          Query Match 9.1%; Score 105; DB 11; Length 27 Best Local Similarity 23.7%; Pred. No. 0.18; Matches 51; Conservative 22; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 - PGARPPHRGGGRGGGGDAAAPPARGGGGGGKAR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-847-102A-56
Sequence 56, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
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                                                                                                                                    5 AAAAAALCFAALVAVAVCQG--
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Best Local Similarity 23.78
Marches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-56
US-09-847-102A-73
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APPLICANT: Honi, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: Cason, Dennis A.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: WHE and Frizzled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-13032002
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
SOFTWARE PALENTING NATE: 2.002-05-01
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APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Wonsey, Angela M.
APPLICANT: Wonsey, Angela M.
APPLICANT: Anderson, Dustin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: human frizzled8 (Fzd8) US-10-285-976-53
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PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
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Publication No. US20030108963A1
GENERAL INFORMATION:
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Sequence 11, Application US/1023353
Sequence 11, Application US/1023353
Publication No. US20030125285A1
GENERAL INFORMATION:
APPLICANT: HIRABAYARIH, Kazuko
APPLICANT: HIRABAYARIH, Kazuko
APPLICANT: HIRABAYARIH, Kazuko
APPLICANT: YANO, Junichi
TITLE OF INVENTION: Method of examining the efficacy of therapy with nucleic acid
FILE REFERENCE: B-345
CURRENT PELLING DATE: 2002-12-19
FRIOR APPLICATION NUMBER: US/10/233,553
CURRENT FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 11
LENGTH: 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 SGGGGGGGGGSSGYG-----SYYQGDNYNSPVPPKHAGKKQ 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 TGGGGGGGGGGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRG--YEEAMPPLEKG-WW 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  736 PHGGQQKPSYGSGYQSHQGQQQSYNQSPYSNYGPPQGKQKGYNHGQGSYSYSNSYNSPGG 795
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Best Local Similarity 25.7%; Pred. No. 1.3;
Matches 43; Conservative 5; Mismatches 35; Indels 84; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 894;
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Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO

APPLICANT: SUMA, MAKIKO

APPLICANT: ARIYAMA, YUTAKA

APPLICANT: ARIYAMA, YUTAKA

TITLE OF INVENTION:

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT PILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER: OF SEQ ID NOS: 2430

SEQ ID NO 670

LENGTH: 544
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LOCATION: (402)...(435)
COTHER INFORMATION: Variable amino acid
US-10-017-161-670
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
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US-10-233-553-23

US-10-233-553-23

US-10-233-553-23

US-10-233-553-23

Sequence 23, Application US/10233553

Publication No. US2000125285A1

GENERAL INFORMATION

APPLICANT: HIRABAYABHI, Kazuko

APPLICANT: HIRABAYABHI, Kazuko

APPLICANT: TANO, Junichi

TILIE OF INVENTION: Method of examining the efficacy of therapy with nucleic acid

FILE REPRENCE: B-345

CURRENT APPLICATION NUMBER: US/10/233,553

CURRENT FILING DATE: 2002-12-19

PRIOR FILING DATE: 2001-09-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 RLPEQGNPDTLCMDYNRTDLTTAAPSPPRRLPPPPPG------EQPPSGSGHGRP--- 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 PHGGÓGKPSYGSGYQSHQGQQGSYNQSLYSNYGPPÓGKQKGYNHGQGSYSYSNSYNSPGG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AAAASAKELACQEITVPLCKGIGYNYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 Q-----FRWGTGLRARCY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EVER-QRLRDLQCWQEV 41
                                                                                                                                                                                                                                                                                                                                                                                                     70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Indels 84; Gaps
                                                                                                                                                                                                                                                                                                                                                  Query Match 9.1%; Score 105; DB 15; Length 694; Best Local Similarity 23.7%; Pred. No. 0.44; Matches 51; Conservative 22; Mismatches 72; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SRPGEGYGQGGQRQMYPPCRPGTTGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 101; DB 15; Length 591; 25.7%; Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 GGGSDYNYESKFNYSGSGGRSG-GNSYGSGG--ASYNPGSHGGYGGG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 YPCSR-PGEGYGYGQGGQRQMYPPCRPGTTGGGPR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 - PGARPPHRĠĠĠĠĠĠĠĠŊAAPPARĠĠĠĠĠĸAR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
; PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
; PRIOR PELICATION NUMBER: 60/341,746
; PRIOR PILING DATE: 2001-12-12
; PRIOR PILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEO for Windows Version 4.0
; SEQ ID NO 144
: LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                     S AAAAAALCFAALVAVAVCQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 GGGGGYYPC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.7
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 SGGGGGGGGSSGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 31
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TYPE: PRT
7 ORGANISM: Homo sapiens
US-10-233-553-23
                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     JS-10-205-823-144
                                                                                                                                                                                                                                                       TYPE: PRT
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102 YEEAMPPLEKGW-WPWGROOOPPP---OGG--GGGOGGYYYPCSRPGEGYGYGOGGOROM 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 623
                                                                                                                                                                                                                                                                                                      , TYPE: PRT
, ORGANISM: Streptomyces avermitilis
US-10-156-761-11120
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.5%;
Best Local Similarity 38.1%;
Matches 37; Conservative (
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CURRENT APPLICATION NUMBER: US/10/029,180
CURRENT PILING DATE: 2001-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 302
------PRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEA 105
                                             106 MPPLEKGWWPWGRQQQPPPQGGGGG------OGGYY-----YPCSRPGEGYGYG 148
                                                                                                                          64 GGVGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWPWGRQQQPP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------QPYSPAYPHSQA--P-GGYAQPP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 POGGGGG-------OGGY----YYPCSRPGEGYGYGQGGQRQMYPPCRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 PÓGQYGGYSQPGPGYGSPAPYSSGQQQGYGSAPYPPSSQASGSYGQQQYGQR---PGSQP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 8.5%; Score 97.5; DB 14; Length 302; I Similarity 25.7%; Pred. No. 0.87; 49; Conservative 16; Mismatches 57; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 EVERORL-----RDLQCWQEVQESPLDACRQVLDRQLTGG---
                                                                                                                                                                                                             149 Q-----GGQRQMYPPCRP 161
                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/10029180
Publication No. US20020182708A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milna, G. Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GTTGGGPRIGR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYPGOOPPYGO 298
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cali, Brian M.
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 49; Conserv
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US-10-156-761-11120
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21; Gaps

33; Indels

Score 97.5; D Pred. No. 1.8; 6; Mismatches

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GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
APPLICANT: PHILLIPPE, Michel
APPLICANT: ARRAUDEAU. Jean-rietere
APPLICANT: ARRAUDEAU. Jean-rietere
APPLICANT: ARRAUDEAU. Jean-rietere
TITLE OF INVENTION: COSMETIC ON DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6188-0165-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 1099-02-11
FRIOR APPLICATION NUMBER: FR 98/01614
FRIOR APPLICATION NUMBER: FR 99/01614
FRIOR APPLICATION NUMBER: FR 99/01614
FRIOR APPLICATION NUMBER: 1998-02-11
SPIOR FILING DATE: 1998-02-11
SEQ ID NO SEQ ID NOS: 14
SEQ ID NO 2.
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 RQLTGGGGGGGGGGPFRWGTGLRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWW 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115. PWGRQQQPPPQGG------GGGQGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 QQGPGGYGPGQQGPGRYGPG-----QQGPSGPGSAAAAAAGSGQQG-PGGYGPRQQGPG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.5; DB 9; Length 529;
Pred. No. 1.9;
9; Mismatches 54; Indels 21; Gaps
156 YPPCRPGT----TGGG---PRIGRVRLTKAREYAAGL 185
                                                      128 OPPOFPGAPTPPPGGGSKNPFKGRPAVLIAAAVAAAL 164
                                                                                                                                                                                                   Sequence 2, Application US/09861597
Patent No. US20020064539A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 8.4%;
1 Similarity 32.8%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Nephila clavipes
US-09-861-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 TTGGG 167
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Sequence 11120, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRWANA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI

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2080 AAAAAAACAAAACAAACAA------AAAAAAGAC-----ATGGGAGA 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GVGPPRWGTG-LRMRCCQQLQDVSRECRCAAIRSMVRGYEEAMPPLEKGWWPWGRQQQPP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AAAAAAALCFAALVAVAVCQGEVERQRLRDLQCWQEVQESPLDACRQVLDRQLTGGGGGG 64
                                                                                                                                                                                                                                                                   APPLICANT: Pan, Janes
APPLICANT: Mathaber Sanith, Victoria
APPLICANT: Watanaber Colin K.
APPLICANT: Watanaber Colin K.
APPLICANT: Watanaber Semin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 59
LENGTH: 2331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.4%; Score 96; DB 15; Length 2331;
25.6%; Pred. No. 9.1;
tive 2; Mismatches 56; Indel8 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2118 GA---TGGTGTTTTTCC-----TCTCCACCACC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2143 -TGGGGATA----CGATGAGAAGATGGCCACCTGCAAGCCAGG 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 POGGGGGGGYYYPCSRPGEGYGYGQGGQRQMYPPCRPGTTGGG 167
RESULT 15
US-10-184-644-59
Sequence 59, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
                                                                                                                                                                        Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.6%
Matches 42, Conservative
                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-59
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APPLICANT:
APPLICANT:
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Search completed: November 29, 2003, 17:11:45 Job time : 49 secs

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Compugen Ltd.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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OM protein - nu	OM protein - nucleic search, using frame plus p2n model
Run on:	November 29, 2003, 17:07:10 ; Search time 271 Seconds (without alignments) 2051.971 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-053-410-4 1148 1 MAKIAAAAAAALCFAALVAVMMCRLSEPQECSIFSGGDQY 206
Scoring table:	BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 0.5 Fgapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0
Searched:	2552756 seqs, 1349719017 residues
Total number of	Total number of hits satisfying chosen parameters: \$105512
Minimum DB seq . Maximum DB seq	Minimum DB seq length: 0

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-Q=CGGD1\_1VGFVD = p20.model -DEV=x1h
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-Q=CGGD1\_1VGFVD = p2001/US1D053410/runat\_28112003\_140756\_278746\_1\_1\_LCOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGGN=200 -THR\_SCORE=EDCT -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15
-USER=US10053410\_@CGN\_1\_1\_0\_@runat\_28112003\_140756\_27874 -NCFU=6 -ICFU=3
-NOM MAAP -LARGEQUERS -NGF\_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DBU\_TIMEDUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries parameters: Command line

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

	Description	vod-G vol	× 2	S ANG	מליינה	Michologide appropri	Micromonospora DNA	Drosophila melanog			Gene #2353 used to	immunodefi	Thermus thermophil	Thermus thermophil	Human protein PP13	Human musculoskele		Nucleotide sequenc	CDNA	Human immune/haema	F	Genomic sequence #	reproductiv	Human testicular a		ays vivipard	osteoplas	Human mila kno tar	mischilosk	O)	Mouse DNA demethyl	Human von willebra	Drosophila melanog		Mycobacterium tube		n		Human excretory re	٠.	Human colon cancer	nucleot	muscle	Human coding seque	equen
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ALIGNMENTS AAV20662 standard; DNA; 2296 BP. 23-JUN-1998 (first entry) AAV20662;

Barley, D-hordein, DPP3, promoter, gene expression, regulation, seed, structural gene, ds. Barley D-hordein gene 5'-terminal region. Hordeum vulgare. AAV20662
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
95 IleArgSerMetValArgGlyTyrGluGlu--
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                                                                                                                                                                                                                                                                                                                                                                            AAF63380 standard; cDNA; 2380
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Best Local Similarity:
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                                                                                                                                                                                                                                                                   The present sequence represents the 5'-terminal region of the barley D-hordein gene. The present invention describes gene expression regulatory DNA which comprises a promoter region derived from the barley (Hordeum vulgare) D-hordein gene which allows expression of a desired structural gene, and a regulatory region regulating such expression. The introduction into plants of expression cassettes containing the gene expression into plants of expression cassettes containing the gene expression into plants of expression of a gene within a plant cell expression vectors) enables the expression of a gene within a plant cell ergions in the regulatory DNA allows control of expression by e.g. tissue type or developmental stage, whilst the use of only an activating regions in the regulatory DNA allows control of expression by e.g. tissue type or developmental stage, whilst the use of only an activating region maintains expression at a high level, providing an effective production means when recovery of the product of the structural gene is desired. The expression cassette/vector may be introduced into e.g. maturing seed andosperm tissue or regeneratable plant calls (e.g. derived from anthers) to improve seeds of barley or other plants, to produce gene products in seeds or to contribute to plant breeding programmes. The expression regulatory DNA can also used in expression systems in vitro. GUS activity in barley protoplasts transfected with plasmid to be paraged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACAGCTG--------GTTGGCCAGCTGCCATGGAGCACGCGGG 246
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                                                                                                                                                                       Gene expression regulatory DNA, expression cassettes and vectors - comprising promoter region from barley, Hordeum vulgare, D-hordein gene, useful to control expression of desired gene e.g. to improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2296 BP; 629 A; 708 C; 606 G; 353 T; 0 other;
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                                                                                                                 Kuroda
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                                                                                                               Ito K, Kihara M,
                           97WO-JP02526.
                                                       96JP-0193433
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                           22-JUL-1997;
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29-JAN-1998
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                                                             307 CTCAGCCAGGTCGTGAGGCAATACGAGCAGCAAACCGAGGTGCCATCCAAGGGAGGATCC 366
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                                                                                                                                                                                                                                                                                                                                                                                                             -----GlnProProProGlnGlyGlyGlyGlyGlyGlnGlyGly 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 TyrTyrTyrProCysSerArgProGlyGluGlyTyrGlyTyrGlyGlnGlyGlyGlnArg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barley, gel protein, D-hordein, malt, wort filterability, extraction, 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 Gln-----MetTyrPro------ProCyBArgProGlyThrThrGlyGly 166
                                                                                                                                                                      367 TTCTACCCGGGCGGGACCGCACCGCCCCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 TCAACTITCCCG---CAGCAGCCAGGACAAGACAA------CAACCAGGACAAGAGG
                                                                                                                                                                                                                                                                       ----ProTrpGlyArgGlnGln-----
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regulator

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This invention relates to barley having a low gel protein content. The barley is transformed with a polynucleotide sequence which regulated the formation of D-hordein. Transformation results in the production of barley strains with improved malting properties such as wort filterability and efficiency of extraction. The present sequence represents cDNA involved in the regulation of D-hordein production.
                                    Transformation of barley with a D-hordein expression production of barley with lowered gel protein content
                                                                                                   Claim 4; Page 31-33; 40pp; Japanese.
WPI; 2001-191587/19
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ProTrpGlyArgGlnGln----- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        474 CACCAAAGCGTAACTTCCTTCCCAGCAGCCAGGACAAGGGCAAGGGTCCTACCCAGGT
                                                                                                                                                                                                                                                                                                             ArgGlnLeuThrGlyGlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGly
                                                                                                                                                                                                                                                                                                                                                       MetAlaLysIleAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleArgSerMetValArgGlyTyrGluGlu-----
                   x AAF63380 (1-2380)
                                                                                                                                        AlavalCysGlnGlyGluvalGlu---
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                 US-10-053-410-4 (1-206)
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367 TTCTACCCGGGCGGGACCGCACCGCCGCTGCAGGAGGAGGATGGTGGGAACCTCTGTA 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                    651
                                                                                                                                                                                                      MetAlaLysIleAlaAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaVal
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Sequence 2434 BP; 675 A; 757 C; 626 G; 376 T; 0 other;
                                                 2434
79
22
51
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 IleArgSerMetValArgGlyTyrGluGlu-------
                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                   x AAF63379 (1-2434)
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ID AAI70852 standard; DNA; 1302
                                            1.21e-08
281.50
46.12%
36.07%
                                                                                                                                                                     US-10-053-410-4 (1-206)
                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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155 MetTyrProProCys----ArgProGly 162
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                                                                                                                   109 LeuGluLysGlyTrpTrpPro-
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140 -----
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                                                                                                                                                                                                                                                                                                                                        A new nucleic acid comprising a variant allele of the 1Ax2asteriskHWW glutenin subunit gene of wheat has at least one extra cysteine codon and is useful for developing new wheat varieties with enhanced quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AlaLeuCysPheAlaAlaLeuValAlaValAlaValCysGlnGlyGluValGluArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 ArgleuArgAspleuGinCysTrpGinGluValGinGluSerProLeuAspAlaCysArg
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the coding region of a newly identified allele, designated lAxZasteriskB, of the lAxZasterisk HWM glutenin subunit gene, found in certain lines of wheat variety Bankuti 1201. The variant differs from the lAxZasterisk gene by a single point mutation of C to G at nucleotide position 1181. This results in a change from Ser to Cys at amino acid position 394. Because of this, the newly identified allele provides enhanced possibilities for the formation of disulfide bridges compared with the known allele, and this could at least partly explain the good technological properties of the variety. The newly identified gene can be used to develop transgenic wheat varieties with better quality gluten.
                                                                          Wheat; glutenin; storage protein; variant; transgenic plant;
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62
17
43
128
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Mismatches:
Indels:
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Matches:
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                                                                                                                            Location/Qualifiers
replace(1181,C)
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                                                                                                                                                                                                                                    14-APR-2000; 2000HU-0001563.
                                                     glutenin gene variant
                                                                                                                                                                                                                                                                             Bedo
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156.00
31.60%
24.80%
13.59%
                               (first entry)
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Tamasne Nyitrai E;
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P-PSDB; AAM50386.
                                                                                                        Triticum aestivum.
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Best Local Similarity:
                                                                                                                                                                     WO200179477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                               18-FEB-2002
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          AAI 70852;
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                                                                                     gluten;
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allele
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                                                     Wheat
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91 ArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGlu-----AlaMetProPro 108
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144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GluGlyTyrGlyTyrGlyGlnGly--------GlyGlnArgGln 154
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595 CAAGGGCAACTAAGACAAGGACAACAAGGTCAGCAGTCAGGACAAGGGCAACCAAGA 654
                                                                                                        ----caccaccrccadaccrracccccagic 174
                                                    90
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                                                       71 TrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArgGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 CCATGGCAGCCAGAACAATTGCAACAACCAACAAGAGGCAACAAGAAGACAGCAACAGGA
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/product= "Synthetic HMW-glutenin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of Synthetic HMM-glutenin construct.
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448 GGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 CAGCAGCTGCGTGACATCTCTCCGGAATGCCACCCGGTTGTTGTTCTTCCGGTTGCTGGC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyTyrGluGlu-----AlaMetProProLeuGluLysGlyTrpTrpProTrpGlyArg 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||:::
154 CAGTACGAACAGCAGATCGTTGTTCCGCCG-----AAAGGTGGTACCTTCTATCCGGGT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GlnGlnGlnProProProGln-------GlyGlyGlyGlyGlyGlnGly 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GAAACCACTCCGCCGCAGCAGCAGCAGCGTATCTTCTGGGGCATCCCGGCTCTGCTG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 GlyTyrTyrTyrPro-----CyaSerArgProGlyGluGlyTyrGlyTyrGlyGln 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 GlyGlyGlnArgGlnMetTyrPro------ProCysArgProGlyThrThr--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 -----CAGGTTTCTTACTACCCGGGTCAGGCTTCTCCGCAGCGTTCTAGTTCTTAC 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GAAGGTGAAGCGTCTGAACAG-------CTGCAGTGCGATCGCGAACTGCAGGAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ValGlnGluSerProLeuAspAlaCysArgGlnValLeuAspArgGlnLeuThrGlyGly 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCys 80
                                                                                                                                                                                                                                                                                                                             This nucleotide sequence is of the synthetic HWM-glutenin construct which is introduced into the DNA of the cereal to form a non-natural repetitive domain which changes the viscoelastic property of a dough. The domain comprises HWW glutenin subunit repeats which are synthetic in sequence or non-natural in number. The dough is useful for making a wheat flour, wheat dough, bread or noodle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaGlyLeuProMetMetCysArgLeuSerGluProGlnGluCysSerIlePheSerGly
                                                                                                                                                                          A process for altering the visco:elasticity of a dough - comprises genetic engineering of a high molecular weight glutenin subunit containing a non-natural repetitive domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AAGCGCTACTACCCGTCTGTTACTTGTCCGCAG------
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73
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Matches:
Conservative:
Mismatches:
Indels:
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130.50
37.62%
27.23%
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Best Local Similarity:
Query Match:
DB:
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Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
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complement (13027..13030)
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complement (12108..13022)
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                                                                                                                                                                                                Micromonospora carbonacea var. africana
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complement (1490..2611)
                                                                                                                                                                                                                                                                             complement (1389..1394)
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                                                                                                                                                                                                                                      complement (132..1382)
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product= "EvdJ"
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product= "EvdA"
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                                                    AAS08693 standard; DNA; 109519
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CDS	CDS	CDS   1937420906   / ttag=	CDS 2274824172 /*tag= ac / product= "EvrG" RBS 2273622740 /*tag= ad /*tag= oduct = "BvrH" /product = "BvrH" /tag= /*tag= ag /*tag= ag /*tag= ag	/product= "Evrl" 26685.30479 /*tag= ah /product= "EvrJ" 2667226676 /*tag= ai complement (3055731876)	30rK" (31885) (31941) (313167)	EVEN" (34419 (34449 EVEN" (35219	/*tag= ap complement (3529436238) /*tag= aq /product= "EvrO" complement (3523536963) /*tag= ar /product= "EvrP" complement (3699838026) /*tag= as /product= "EvrO"	complement (3807238566) /*tag= at /product= "EvrR" complement (3889240163) /*tag= au /product= "EvrS"	

CC cell-cell interactions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA cequences (ABL01840-ABL16175) and the encoded proteins corpused (ABL01840-ABL16175) and the encoded proteins corpused (ABL01840-ABL16175) and the encoded proteins corpused (ABL01840-ABL16175) and the encoded proteins corpused corpused for this patent did not form part of the printed corpused for this patent did not format directly from WIPO corpused corpused for the sequences.  CC ABBS7737-ABB72072)  CC ABBS7737-ABB72072)  CC ABBS7737-ABB72072)  CC ABBS7737-ABB72072)  Alignment Scores:  Alignment Scores:  Alignment Scores:  Alignment Scores:  Brecont Similarity:  CC ABBS774-ABB72074  Alignment Scores:  Brecont Similarity:  CC ABBS774-ABB72074  Alignment Scores:  CC ABBS774-ABB72074  Alignment Scores:  Brecont Similarity:  CC ABBS774-ABB72074  Alignment Scores:  CC ABBS774-ABB72074  Alignment Scores:  Alignment Alignment Scores:  Alig	Oy 6 AlaAlaAlaAlaAlaLeuCygPheAlaAlaLeu	34 AspleudlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArgGlnValLeu 53  [  :::   ::   ::    ::     ::	150	Qy         101 -GlyTyrGluGluAlaMetProFroLeuGluLysGlyTrpTrpProTrp- 116           Bb         312 CAACCGTCAGCAACCGACCCTCCTGGCTGGCCACCGGCTGGCAGTGGGG 362           Qy         117GlyArgGlnGlnGlnPro	Qy         143 uGlyTyrGlyTyrGlyGlnGlyGlnAegGlnMetTyrProProCysArgProGlyTh 163           Db         459 TGGTCCAGGATGGAACGGAGGGCGGTGGAAGAGACCTCCACCAAGACCAGGTTT 512           Qy         163 TThrGlyGlyPro 168           Db         513 TAACGGCGGCGGACCA 528           RESULT 8           ABL12130	ID ABL12130 standard; cDNA; 3089 BP.  XX AC ABL12130;  XX DT 26-MAR-2002 (first entry)  XX
Oy         55 ArgdlnLeuThrdlyGlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGly         74           Db         87615 ACGCGGCGATCGACCGCTGGTACCGGGCTGGTCG	Qy 139 rArgProGlyGluGlyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMe 155	166	ABL12131; Brandard; CDNA; 1083 ABL12131; 26-MAR-2002 (first entry) Drosophila melanogaster expres	KW pharmaceutical; gene; ss.  XX OS Drosophila melanogaster.  XX XX XX XX XX XX XX XX XX XX XX XX X	XX XX XX XX PI Venter JC, Adams M, Li PWD, Myers EW; XX XX XX DR WPI; 2001-656860/75. DR P-PSDB; ABB68028. XX YX YX YX YX New isolated nucleic acid detection reagent for detecting 1000 or more PT genes from Drosophila and for elucidating cell signalling and cell-cell PT interactions -	

143

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1252 AGGAAGGCCGGGGATGGGTCCGAATCGAGGAATGCACAGGACCAGGATTTGCACCACC 1311
                                                                                                                            1312 CAACCGTCAGCAACCGACGCCTCCT-----GGCTGGCCACCCGGCTGGCAGTGGGG 1362
                                                                                                                                                                                                            1363 AGCCGGTGGAATCAGAATCAACCCGGATTTGACTGGGTTCAAACAGGATTTGCACCAGG 1422
                                                                                                                                                                                                                                                                                               -----CCAGGATGGAA 1458
                                                                                                                                                                                                                                                                                                                                                                               1459 TGGTCCAGGATGGAACGGAGGCGGTGGAAGAGGA-----CCTCCACCAAGACCAGGTTT 1512
  GlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValArg 100
                                                                                                                                                                                                                                                                                                                                          143 uGlyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyrProProCy8ArgProGlyTh 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an Oligo-dr primer and an Oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an Oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                        124 oglnGlyGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrProCysSerArgProGly---Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito K, Yo
                                                                                                                                                                       -----GlyArgGlnGlnGlnPro------GlyArgGlnGlnPro-
                                                                                    101 -GlyTyrGluGluAlaMetProProLeuGluLysGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 17756; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nikawa T, Hayashi K, Sa
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:17756.
                                                                                                                                                                                                                                                                                                 1423 CTGGAATGGAGGTGGAGGGCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽.
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T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1513 TAACGGCGGCGGACCA 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH17970 standard; cDNA; 1847
                                                                                                                                                                                                                                                                                                                                                                                                                             163 rThrGlyGlyGlyPro 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
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Ishii S,
                                                                                                                                                                       117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1066 CTGGATACGCACGTGTCTCGCGCAATTTGCAGTCTCCTCGTCCTCGCCGCGGGGGCTGT 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GGTGGCCCAGCTGCCCGGTTTCGGAGTTATCAATGGACTGAT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1192 CAATGCCATGCACAACAACAACGCTTCAACCAGCAGCGCGGAGTTĆĠAGAGACTGCAGCA 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AspArgGlnLeuThrGlyGlyGlyGlyGlyGlyGlyValGlyProPheArgTrp---- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GlyThrGlyLeuArgMetArgCysCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ecification, but was obtained in electronic format directly from WIPO ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------ValAlaValAyaGlnGlyGluValGluArgGlnArgLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 AspleuGlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCysArgGlnValLeu
  melanogaster expressed polynucleotide SEQ ID NO 30872
                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 30872; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3089 BP; 819 A; 769 C; 725 G; 776 T; 0 other;
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16
61
74
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeu-
                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.4
127.50
34.47%
26.70%
11.11%
                                                                 pharmaceutical; gene; ss
                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-053-410-4 (1-206)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB68027
                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                           27-SEP-2001
Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
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polynucleotide which comprises a 3'-end sequence, where the obligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and particularly full-length conva. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH30166 to AAH13628 and AAH13633 to AAH13612 represent human anino acid sequences; and AAH3362 to AAH13632 represent coligonal colides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                  the present invention.
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Sequence 1847 BP; 467 A; 505 C; 431 G; 444 T; 0 other;

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Alignm Pred. Score: Percen Best L Query	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	27.4 126.50 13.93\$ 33.70\$ 11.02\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1847 . 62 117 145 9	
US-1	US-10-053-410-4 (1-206)	x AAH17970 (1	-1847)		
ò	18 ValAlaVa	lAlaValCysGlnGly	GluValGluArgGlnA	ValalaValAlaValCysGlnGlyGluValGluArgGlnArgLeuArgAspLeuGlnCys	37
g	   1550 GTGGAGGT	i Ggaggaatgccagggc	::: :CTCCGGGAAATGGAGG	 	1491
ò	38 TrpGlnGl	uValGlnGluSerPro	Leu-AspAlaCyșArg	TrpGjnGjuValGlnGjuSerProLeu-AspAlaCyeArgGlnValLeuAspArgGlnLe	57
q	1490 CACCAGGA	 caccaggaaggaaggaggaggaggaggataccattcctgc	::: GTGGCATTCCTGC	TTCTCCAGGCAAGG	1440
ò	57 uThr-Gly	uThr-GlyGlyGlyGly		-GlyGlyGly-ValGlyProPhe	69
QQ	1439 GAGGAGGT		  cactcccaggcaaagg	GAGGAGGTGGGGGGGAATTCCAGCACTCCCAGGCAAAGAAGGGGGTGGTGGTGGTGGTGGTTCT	1380
ò	04	Arg	TrpGlyThrGlyLeu	-ArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGln	82
ପ୍ର	1379 AGCACTCC	  CAGGCAAAGGAGGAGG	 TGGGGGATGGCAGTA	AGCACTCCCAGGCAAAGGAGGAGGAGGGATGGCATACCTCCAGGCAAAGAAGAGGGGGATGGCAGTACCTCCAGGCAAAGAAGAAGGAGGGGATGGCAGTACCTCCAGGCAAAGAAGAGGGG	1320
ò	83 LeuGlnAspValSer	pValSer	ArgGluCys	-ArgGluCysArgCysAlaAlaileArgSer	97
g	1319 TGAAGGGA	 TGCCAACACCCTCAGG	  CAAAGGAGGGGTGGP		1260
ò	98 MetValArg	913	aMet ProProLeuGlu	Tyr-GluGluAlaMetProProLeuGluLysGlyTrpTrpProTrpGl	1117
qq	1259 CAAAGGAG	CAAAGGAGGGGTGGAGAGATAGCAGTACCTCCAGGTAAAGAAGGG			1212
ò	117 yArgGlnG	yArgGlnGlnGlnBroProPro-	-GinglyGlyGlyGly	Ginglyglyglyglyglyglyglyglyryrryr	136
g	1211 TGAGGAGA		:::		1160
ò	136 rProCysS	rProCysSerArgProGlyGluGlyTyrGlyTyr-	YTYrG1XTYr	GlyGlnGlyGlyGl	152
q	1159		  AGGAGGAGTGGTACTA	-dgaggaggaggaggggggggaggggggggggggggggg	1116
ò	152 nArgGlnM	nArgGlnMetTyrProPr	oCysArgProGlyThr	-ProCysArgProGlyThrThrGlyGlyGlyBroArgll	170
đ	: 1115 TGGAATAA	TAGTGCCAGAGTCACC	 	TGGAATAATAGTGCCAGAGTCACCAGGTAAAGGAGGGCCAGGGGGAACAGGAGCACGACT	1056
ò	170 eGly 171	•			
අු	1055 AGGA 1052	5			
RESULT ABN958 ID A	RESULT 10 ABN95855/c ID ABN95855 standard;	l; DNA; 2042 BP.			
<b>\$</b> \$	ABN95855;				
ž E	13-AUG-2002 (first	st entry)			

Gene, liver cancer; ds; hepatocellular carcinoma, hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism. Gene #2353 used to diagnose liver cancer.

Homo sapiens

WO200229103-A2

11-APR-2002.

02-OCT-2001; 2001WO-US30589.

02-OCT-2000; 2000US-237054P.

(GENE-) GENE LOGIC INC

Vockley JG; Horne D, Alvares C, Peres-Da-Silva S,

WPI; 2002-426119/45.

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in liver tissue sample

Claim 1; SEQ ID NO 2353; 298pp; English.

progression of liver cancer, here accellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO The invention relates to a novel method for diagnosing and detecting the at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 2042 BP; 326 A; 755 C; 611 G; 350 T; 0 other;

2042 54 10 47 90 Length; Matches: Conservative: Mismatches: Indels: 39.9 124.50 31.84% 26.87% 10.84% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: .. 0

US-10-053-410-4 (1-206) x ABN95855 (1-2042)

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48	48 AlaCysArgGlnValLeuAspArgGlnLeuThrGlyGly-GlyGlyGlyGlyGlyValGl 67	
899		
67	67 yProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSe 87	
848		
87	87 rArgGluCysArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGluAlaMetPr 107	
832	TGGGCGAGAGAAAGACCCACACCTGTC 804	
101	107 oProLeuGluLysGlyTrpTrpTrpTrpGlyArgGlnGlnGlnGlnProPro 123	
803	803 TCCTCTCAGCAACTCCCGGGGCGCCTGGGCAACTCCCCGTGCCCACCGCCCCATGGA 744	

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Claim 40; Fig 8B; 65pp; English.

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-----ProGlnGlyGlyGlyGlyGlyGlnGlyGlyTyrTyrTy 136
                                                                                                                                                                                                                                                                                                                                                                                                                              563 GGGATTCGGCTTGGGTGCTGCATGCCGGAGGAAGGGCGGCCTCTCATACCCGCTCCCC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 AGTCGGGGGAGGGCGCCTTAGAGGGGCGATGCCGGGTCAGGAGGTCGCTCGGGGTCGTCC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel immunogen for stimulating anti-HIV immune response, has a portion of gag protein of HIV from HIV clade, parts of p17, p24 and synthetic polypeptide comprising human cytotoxic T-lymphocyte epitopes of HIV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GlyProArgIleGlyArgValArgLeuThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 GCGGGGGGGTCGTTGGGCTCCTGGGGCTGGGAGACTCCGGATTGCGGGAGG
                                                            ------LysAlaArgGluTyrAlaAlaGlyLeuPr
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gene therapy; fusion protein; modified vaccinia virus Ankara vector;
MVA; cytotoxic T-lymphocyte; CTL; epitope; ds.
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14-OCT-2000; 2000GB-0025234.
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The invention relates to human immunodeficiency virus immunogens and their corresponding DNA molecules. An immunogen comprises a portion of aga protein of HIV from an HIV clade, parts of p17 and p24, modified to prevent N-terminal myristoylation; and a synthetic polypeptide comprising human cytotoxic T-lymphocyte (CTL) epitopes of HIV protein. This municipan is designed to elicit an HIV-pepcific immunogen. This comprises of HIV protein. This communogen is useful in the preparation of a medicament such as vaccine to prevent or treat HIV infection in a human subject.

The invention also relates to method of stimulating anti-HIV immune response in a human subject which comprises administering one or more times an amount of nucleic acid molecule sufficient to prime an immune response to the immunogen, or else may be packaged within a delivery means, such as a modified vaccinia wirus Ankara (WAA) to boost the immunocer cesponse to common portion of the immunogen. The HIV A immunogen consists of about 73 of gag protein fused to a string of 25 partially consists of about 73 of gag protein fused to a string of 25 partially coverlapping human CTL epitopes. The gag domain of HIV A contains p24 and p17 in an order reverse to the viral gag p17-p24-p15 polyprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ22143 to ABZ22146 encode the Thermus thermophilus DNA repair enzymes MutY, RecJ, RecF, and TRCF given in ABP56413 to ABP56416. The enzymes can be used as research reagents for biochemistry and molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DNA repair enzyme gene, a protein, a recombinant vector, a transformant, preparation of DNA repair enzyme, repairing the error sequence of a DNA, and prevention of error synthesis of a DNA sequence
                                   1094 AGGGCATGACCCTCGCCAACCTCACCGTGGAGGCGGGGGCCAAGGCGGGGGCTCGTGCTC
                                                                     ---MetMetCysArgLeuSerGluProGlnGl
                                                                                                                                                                                                                                                                                                                                               Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                  Thermus thermophilus; DNA repair enzyme; enzyme; MutY; RecJ; RecF; RRCF; biochemistry; molecular biology; research; gene; ds.
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                                                                                                                                        196 uCysSerllePheSerGlyGly 203
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                                                                     181 rAlaAlaGlyLeuPro----
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   gValArgLeuThrLys---
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P-PSDB; ABP56415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the genomic DNA region from Thermus thermophilus which contains the coding regions for the L-lysine biosynthetic protein homoaconitase hydratase subunits I and II. The gene can be used for the generation an L-lysine-producing Thermus thermophilus strain for the production of L-lysine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 AlaIleArgSerMetValArgGlyTyrGluGluAlaMetProProLeuGluLysGlyTrp 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 GlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArgGluCysArgCysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 TrpProTrpGlyArgGlnGlnGlnProProProGln-GlyGlyGlyGlyGly-----Gl
                                  L-lysine biosynthesis; homoaconitase hydratase; ds.
                                                                                                                                                                                                                                                                                                                             L-lysine biosynthetic system gene of Thermus genus microbe
thermophilus homoaconitase hydratase gene region.
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Mismatches:
Indels:
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                                                                  Thermus thermophilus
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                                                                                                                                                                                                                                                                                                                                                  672 cercial acceaecca de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de consta
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                        LeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValArgGlyTyr 102
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                                                               -----ccgctacgacgacgatcgtgccr
                                                                                                               GluGluAlaMetProProLeuGluLysGlyTrpTrpFroTrpGlyArgGlnGlnGlnPro
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1314..2414
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                                            5 AlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaValAlaValCysGln
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                                                                                                                                      25 GlyGluValGluArgGlnArgLeuArgAspLeuGlnCysTrpGlnGluValGlnGluSer
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                                                                     1292 GCCCTGCCGGCACCCCTGCTCTGAGCTGGCCCTCCCTCGTC---
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x ABZ80413 (1-2986)
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2001US-0259678
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27.58P-2000;
29.58P-2000;
29.58P-2000;
29.58P-2000;
29.58P-2000;
29.58P-2000;
20.0CT-2000;
02.0CT-2000;
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02.0CT-2000;
03.0CT-2000;
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2000US-0180664.
2000US-0189874.
2000US-0199076.
2000US-0199077.
2000US-0199077.
2000US-0199076.
2000US-01990767.
2000US-01990767.
2000US-011496.
2000US-021488.
2000US-0215135.
2000US-021689.
2000US-021689.
2000US-021486.
2000US-021486.
2000US-0214518.
2000US-0224518.
2000US-0224518.
2000US-0225267.
2000US-0225267.
                                                17-JAN-2001; 2001WO-US01338
                     WO200155367-A1
        Homo sapiens.
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06-SEP-2000,
06-SEP-2000,
08-SEP-2000,
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14-SEP-2000,
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC. WPI; 2001-451937/48. diagnosis -Rosen CA, 

Example 2; SEQ ID NO 2718; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB03109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment c and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointesfinal tract, liver, lung, or urogenital; (b) immune c discorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 9968 BP; 2324 A; 2302 C; 2695 G; 2647 T; 0 other;

Alignment Scores:			
Pred. No.:	285	Length:	9968
Score:	121.00	Matches:	9
Percent Similarity:	37.57	Conservative:	11
Best Local Similarity:	31.75%	Mismatches:	65
Query Match:	10.54%	Indels:	54
DB:	22	Gaps:	10

US-10-053	-410-4 (1-206)	US-10-053-410-4 (1-206) x AAL36353 (1-9968)
ò	5 AlaAlaAlaA	5 AlaAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaValAlaValCysGln 24
Ωp	900000000000000000000000000000000000000	TGTACCCCGTGTCTGCCGCTGGCGGCCGACGCGCCCTGCTG 148
δ	25 GlyGluValG	luArgGlnArgLeuArgAspLeuGlnCysTrpGlnGluValGlnGluSer 44
q	149 GGCCACATCG	
ò	45 ProLeuAspA	45 ProLeuAspAlaCysArgGlnValLeuAspArgGlnLeuThrGlyGlyGlyGlyGlyGly 64
qq	206	:::
ò	65 GlyValGlyProPheArg	roPheArgTrpGlyThrGlyLeuArgMetArgCysCys 80
qq	233 GCGAG-GGCC	233 GCGAG-GGCCCGGCCGCCGCCAAGGAGGGCGCGGGG
ò	81 GlnGlnLeuG	81 GlnGlnLeuGlnAspValSerArgGluCygArgCygAlaAlalleArgSerMetValArg 100
q	274	
È	101 GlyTyrGluG	lualaMetProPro-LeuGluLysGlyTrp113
QQ	313 6666666	313 GGCCCGGGCCGAAGCCGGCCGTGCGCCTGGAGGACCGCTTCAACAGCATCCCCGC 372
ò	114Trp	TrpProTrpGlyArgGlnGlnGlnFroProProGlnGlyGlyGly 128
අු	373 CGAGCCGCCG	373 CGAGCCGCCGCCGCCGCCCCCGAGCCCCCGAGCCGGGCGCGCTCAACAA 432

rgPr 141	3GCC 483	gar 160	3ccc 543			
129GlyGlyGlnGlyGlyTyrTyrTyrTyrProCysSerArgPr 141	433 GTGCGTGCCCGGGGCCGGGGGCCCGGGTGGAGGCCGAGGCC 483	141 oGlyGluGlyTyrGlyTyrGlyGlnGlyGlnArgGlnMetTyrProProCygAr 160	484 GGGGCCGGGGCCGGGGGGGGGGAGGGGGCCCTCGCTGTGCACGCCCCCAGCCTGCC 543	160 gProGlyThrThrGlyGlyBro 168	544 TCCCGGCGCACAGGGCGCGGACCT 568	
129	433	141	484	160	544	
ò	qq	ò	qq	δ	Dp	

Search completed: November 29, 2003, 17:16:58 Job time : 309 secs

Appli

Scoring table:

Searched:

Seguence:

Run on:

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Sequence 105402, Sequence 105402, Sequence 22, Appl Sequence 2023, Appl Sequence 2, Appl Sequence 2, Appl Sequence 112, Appl Sequence 172, Appl Sequence 174, Appl Sequence 219, Appl Sequence 219, Appl Sequence 219, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Se
                                                                                                                                                                                                                                                            Sequence 140092,
Sequence 140092,
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Sequence 140201,
Sequence 16086, A
Sequence 16086, A
                                                                                                                                      Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2955, Ap
Sequence 2955, Ap
                                    Sequence 748, App
Sequence 4504, Ap
Sequence 3369, Ap
                                                                                                                                                                Sequence 5, Appli
Sequence 2718, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10231, A
Sequence 1145, Ap
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111991
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 115601
Sequence 115601
                                                                                                                                                                                                                               Sequence 1, A
Sequence 8525
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Sequence 1, A
             Sequence 33,
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                                                                                                                                                                                                                                                                                                                                                               Sequence
US-10-168-843A-33

US-10-259-165-748

US-10-156-761-1

US-10-156-761-1

US-09-38-901-5

US-09-764-897-2718

US-09-764-897-2718

US-09-764-897-8718

US-10-027-632-119991

US-10-027-632-111991

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US-10-027-632-115601

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US-10-027-632-116086

US-10-027-632-105402

US-10-027-632-105402

US-10-027-632-105402

US-10-027-632-105402

US-10-027-632-105402

US-10-027-632-105402

US-10-037-632-105402

US-10-037-332-105402

US-10-037-332-105402

US-10-037-3319-712

US-10-038-817-219
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US-09-764-860-1145
US-09-764-846-345
US-09-764-891-7710
US-09-764-891-10231
US-10-10-874-282
US-10-091-483-345
US-10-079-854-282
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JOS-10-126761

Reguence 1, Application US/10156761

GENERAL INFORMATION:

APPLICANT: CMURA, SATOSHI

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, JUN

APPLICANT: SHIKAWA, JUN

APPLICANT: SHIKAWA, HROSHI

APPLICANT: HATTORI WOSHIYWII

APPLICANT: HATTORI WOSHIYWII

APPLICANT: HATTORI WOSHIYWII

APPLICANT: HATTORI WOSHIYWII

APPLICANT: HATTORI WOSHIYWII

APPLICANT: HATTORI WOSHIRA

TITLE OF INVENTION NUMBER: US/10/156,761

CURRENT APPLICATION NUMBER: US 2001-204089

PRIOR PELING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-06-30

PRIOR FILING DATE: 2001-06-30

PRIOR FILING DATE: 2001-06-30

PRIOR FILING DATE: 2001-06-30

SEQ ID NO 1
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TYPE: DNA
ORGANISM: Streptomyces avermitilis
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80557
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707
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1329
7727
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115.5
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-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
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-O=/cgn2 1/USFTO spool/US10053410/runat_28112003_140759_27990/app_query.fasta_1.391
-DB=Published_App_lications_NA -QFMT=fastap -SUFFIX=p2n.mpb -MINMATCH=0.1
-LOOPCL=0 -LOOPERT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62
-TTRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAXIEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pco -NORM=ext -HRAPSIZE=500
-MAXIEN=200000000 -USER=US10053410 @CGN 1 1 271 @runat_2811203 140759_27990
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -AGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                              November 29, 2003, 18:16:16; Search time 311 Seconds (without alignments) 2182.335 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                      1148
1 MAKIAAAAAAALCFAALVAV......MMCRLSEPQECSIFSGGDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '/ Ggn2_G/ptodata/2'pubpna/USO7_PUBCOMB. seq:*
'/ Ggn2_G/ptodata/2'pubpna/PCT_NEW_PUB.seq:*
'/ Ggn2_G/ptodata/2'pubpna/USO6_NEW_PUB.seq:*
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'/ Ggn2_G/ptodata/2'pubpna/USO9_NEW_PUB.seq:*
'/ Ggn2_G/ptodata/2'pubpna/USO8_NEW_PUB.seq:*
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                                          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127.5 11.1 9025608 14 US-10-156-761-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*
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Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                               US-10-053-410-4
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
                                                                    Copyright
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Perfect score:
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Jatabase :

Result 8

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APPLICANT: 2004
APPLICANT: 2004
APPLICANT: Chang, Hur-song
APPLICANT: Cooper, Bret
APPLICANT: Gooper, Bret
APPLICANT: Gooper, Bret
APPLICANT: Gooper, Bret
APPLICANT: Goff, Steven P.
APPLICANT: Goff, Steven A.
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Todd
APPLICANT: Katagiri, Ruicholas
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Moughamer, Todd
APPLICANT: Moughamer, 10cd
APPLICANT: Moughamer, 10cd
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APPLICANT: APPLICANTON NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
MUMBER OF SEQ ID NOS: 1782
MUMBER OF SEQ ID NOS: 1782
MUMBER OF SEQ ID NOS: 1782
MUMBER OF SEQ ID NOS: 1782
                                                                                                                                              2237
                                                                                                                                                                                                                                               2236 AGGGGTTGGACTGGTACAGGATCTTGATGATGCGGATGGCCTTCAGCAGCTCCTCGTCGG 2177
                                                                                                                                                                                                                                                                                                                                               2176 AGTÍGCCGGAGCGGC-----CGGCGTCCTCCGGTCGGTCTCGGTCTTGGACTCCA 2126
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2125 ---ccrrcrrcrrdgacrccrrcggccccrccrccrcccccr-----cccrcrdd 2078
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                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                109 LeuGluLysGlyTrpTrpFroTrpGlyArgGlnGlnGlnProProProGlnGlyGlyGly 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 Gly-------GlyGlnGlyGlyTyrTyrTyrDroCygSerArgProGly 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ---GluGlyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyrProProCygArgPro 161
                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                             89 GlucysArgCysAlaAlaIleArgSerMetValArgGlyTyrGluGluAlaMetProPro
                                                                                                                                            2296 cescececeacescescescescestrerreceseceréscescerescerresserresserresser
                                                                                                                                                                                             73 ThrGlyLeuArgMetArg------CysCysGlnGlnLeuGlnAspValSerArg
                                                                                                -----GlyGlyGlyValGlyProPheArgTrpGly
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LENGTH: 747
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Matches:
Conservative:
Mismatches:
Indels:
                                              US-10-053-410-4 (1-206) x US-10-168-843A-33 (1-4350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 748, Application US/10259165
Publication No. US20030135888A1
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
                                                                                                  55 ArgGlnLeuThrGlyGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       966 AGCACACGGGGCAGTGGT 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 GlyThrThrGlyGlyGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.00475
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31.45%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea
US-10-259-165-748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-259-165-748
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4272208 TGCTGCCGCGTTTCCGC-----TGCTGGCGGCGGCGGTGCCTGAGGCTGCGG 4272164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4272067 GCTGGTCGCGGCCGCGCACACCGCGCGCGCGCGCCACCACCGCTGC---TGTGCGGG 4272011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CGGGGGTGCTGTTG 4272128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4272010 GCCGTTCTCTGGATACTGGCACGCGCTGGCGGCCGCCCCCTCAGGGGTGCGCACGCTGG 4271951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GlyGlyGlyGlyGlyTyrTyrTyrProCysSerAr 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 gProGlyGluGlyTyrGlyTyrGlyGlnGlyGly------GlnArgGlnMetTyrPr 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Medical Research Council
APPLICANT: International Aids Vaccine Initiative
APPLICANT: International Aids Vaccine Initiative
APPLICANT: University of Nairobi
TITLE OF INVENTION: Improvements in or Relating to Immune Responses to HIV
FILE REFERENCE: MJL/C1248'1/M
CURRENT APPLICATION NUMBER: US/10/168,843A
CURRENT FILING DATE: 2002-09-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                   59 GlyGlyGlyGlyGlyGlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÇyşÇyşGlnGlnLeuGlnAspValSerArgGluÇyş-----ArgCyşAlaAlalleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 SerMetValArgGlyTyrGluGluAlaMetProProLeuGluLysGlyTrp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 oProCysArgProGlyThrThrGlyGlyGlyProArglleGlyArgVal 173
                                                                                                                                                                           9025608
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                    NAME/KEY: misc_feature

LOCATION: (4187715)

CHER INFORMATION: a, t, c, g, other or unknown

US-10-166-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 33, Application US/10168843A; Publication No. US20030108562A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4272163 GGCCGTGGGGCTGGGTGG----
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40.88%
30.66%
11.11%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-168-843A-33/c
                                                                                                                                                    Alignment Scores:
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LENGTH: 4350
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124 oGlnGlyGlyGlyGlyGlyGlnGlyGlyTyrTyrTyrFroCysSerArgProGlyGluGl 144
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                                                                                   ----MetValArgGlyTyrGluGlu 104
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                                                                                                                           73 ThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArgGluCysArgCys
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                                          59 GlyGlyGlyGlyGlyGlyValGlyProPheArgTrp-
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Matches:
Conservative:
Mismatches:
US-10-053-410-4 (1-206) x US-10-156-761-4504 (1-930)
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TILLE OF INVENTION: NOWEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-3
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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Best Local Similarity:
Query Match:
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LOCATION: (1)
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                                                                                            301 GGCGGCGGTCGCAGCTACGGTGGTAGCTGGGGGCGGCGGCCGGAGATCCGGCGGCGGGGGG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
               US-10-053-410-4 (1-206) x US-10-259-165-748 (1-747)
                                                            59 GlyGlyGlyGlyGlyGlyGlyValGlyProPhe---
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, VOSHIYUKI
APPLICANT: HATTORI, WASHIRRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4504, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
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ORGANISM: Streptomyces avermitilis
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Best Local Similarity:
Query Match:
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US-10-156-761-4504
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US-10-156-761-4504
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                                                                                                                                                                                                                                                                                                  PheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeuGlnAspValSerArg 88
                                       30 GlnArgLeuArgAspLeuGlnCysTrpGlnGluValGlnGluSerProLeuAspAlaCys 49
                                                                    --ThrGlyGly-----GlyGlyGlyGlyGlyValGlyPro
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                                                                                                                              Arg------GinValLeuAspArgGlnLeu-------
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US-10-053-410-4 (1-206) x US-10-156-761-3369 (1-1578)
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, HARNOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-26
CURRENT PILING DATE: 200-05-29
CURRENT PILING DATE: 200-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI
APPLICANT: IREDA, HARUO
PREPLICANT: ISHIKAWA, UIN
APPLICANT: HORIKAWA, HIROSHI
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5523477 GGCGGAGGCGGAGGCGGAGCCCGGAACCCGCCGGTTCCGAGGTGACGTCCGATCCGGA 5523536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 oginglyglyglyglyglyglnGlyGlyTyrTyrTyrProCysSerArgProGlyGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5523764 GCAGCGCGGAGGAGGTGGACCACGCGCCCCCCGCGGCCGTTA---CGCCCCGGTCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ThrGlyLeuArgMetArgCysGlnGlnLeuGlnAspValSerArgGluCysArgCys
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| Publication No. US20030008291A1
| GENERAL INFORMATION:
| APPLICANT: Kuramitus Seiki,
| APPLICANT: Yokoyama Shigeyuki
| TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
| FILE REFERENCE: PH-1261-US
| CURRENT APPLICATION NUMBER: US/09/938,901
| CURRENT APPLICATION NUMBER: US/09/938,901
| PRIOR PRIOR PILING DATE: 2001-02-23
| NUMBER OF SEQ ID NOS: 17
| SOUTWARE: PATCHIN VOET: 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                           other or unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 rGlyGlyGlyProArgileGly 171
ORGANISM: Streptomyces avermitilis
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122.00
36.49%
33.78%
                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, t,
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; LOCATION: (1)..(1029)
US-09-938-901-5
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	OY 65 GIYVAIGIYPFOPREATGTIPGIYTRTGIYLEWARGMETAIGCYSCYS 80	Qy 81 GlnGlnLeuGlnAspValSerArgGluCysArgCysAlaAlaIleArgSerMetValArg 100	Oy 101 GlyTyrGluGluAlaMetProPro-LeuGluLysGlyTrp 113	Oy 1141rpProTrpGlyArgGlnGlnGlnProProGlnGlyGlyGlyGly 128	Qy         129	Qy 141 oGlyGluGlyTyrGlyTyrGlyGlnGlyGlnArgGlnMetTyrProProCysar 160	Qy         160 gProglyThrThrGlyGlyGlyPro 168           Db         544 TCCCGGCGCACAGGGCGGGACCT 568	RESULT 9 US-10-168-097A-1/C : Sequence 1. Application US/10168097A		8: 0.0191 Leng 120.50 Matc 120.50 Matc 120.50 Mism 1artry: 35.14% Mism 10.50% Inde 12 Gaps	US-10-053-410-4 (1-206) x US-10-168-097A-1 (1-1806)  Qy 60 GlyGlyGlyGlyGlyGlyProPheArgTrpGlyThrGlyLeuArgMetArgCys 79  Db 1284 GGAGGGGGGGGGTGGGTCCATTCCCGGAGCTGGGGGGGGGG
Alignment Scores:  Pred. No.: Score: Score: 121.00 Matches: Percent Similarity: Best Local Similarity: 33.34\$ Mismatches: 44 Conservative: 7 Best Local Similarity: 10.54\$ Indels: 7 Annels: 11.54\$	11 10-053-410-4 (1-206) x US-09-938-901-5 (1-1029)	Qy         63 GlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGln 82	QY 83 LeuGlnAspValSerArgGluCysArgCysAlaalalleArgSerMetValArgGlyTyr 102	Qy     103 GluGluAlaMetProProProLeuGluLy8GlyTrpTrpProTrpGlyArgGlnGlnGlnPro 122	Qy 123 ProProGlnGlyGlyGlyGlyGlyGlyGlyGlyTyrTyrTyrProCys 138	Oy 139 SerArgProGlyGluGlyTyrGlyTyrGlyGlnGlyGlyGlnArgGlnMetTyrProPro 158	Oy 159 CysArgProdlyThrThrGlyGlyGly	Oy 171 GlyArg 172         :: : Db 792 GGCCAA 797	RESULT 8 US-09-764-877-2718 US-09-764-877-2718 Sequence 2718, Application US/09764877 Patent No. US20020147140A1 HESPERAL INFORMATION: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005 CURRENT APPLICATION NUMBER: US/09/764,877 Prior application data removed - refer to PALM or file wrapper Prior application data removed - refer to PALM or file wrapper SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2718 LENGTH: 9968 LINTER: DNA ORGANISM: Homo sapiens	Alignment Scores:  Pred. No.:  Score: Score: Percent Similarity: Best Local Similarity: 10.54* DB:  Alignment Scores:  121.00 Matches: 60  Conservative: 11  Matches: 65  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 11  Conservative: 12  Conservative: 13  Conservative: 14  Conservative: 16  Conservative: 17  Conservative: 18  Conservative: 19  Conservative: 10  Conservative: 10  Conservative: 10  Conservative: 11  Conservative: 11  Conservative: 12  Conservative: 13  Conservative: 14  Conservative: 16  Conservative: 17  Conservative: 18  Conservative: 19  Conservative: 10  Conservative: 11  Conservative: 12  Conservative: 11  Cons	US-10-053-410-4 (1-206) x US-09-764-877-2718 (1-9968)  Qy 5 AlaAlaAlaAlaAlaAlaAlaAlaLeuCysPheAlaAlaLeuValAlaValAlaValCysGln 24

RESULT 11  US-10-027-632-140092/c  Sequence 140092, Application US/10027632  Sequence 140092, Application US/10027632  Publication No. US20030204075A9  GENERAL INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMER APPLICATION NUMBER: US 60/218,006  PRIOR PRING APPLICATION NUMBER: US 60/18,676  PRIOR FILING DATE: 2000-04-20  PRIOR PELICATION NUMBER: US 60/19,483  PRIOR FILING DATE: 2000-03-29  PRIOR PELICATION NUMBER: US 60/193,483  PRIOR PELICATION NUMBER: US 60/193,483  PRIOR PELICATION NUMBER: US 60/167,363	Alignment Scores:
Db 1232	arity: arity: arity: -4 (1- G1yG1 GGCCAArgse TrpG1 TrGGGC ArgCA ArgCA ArgCAA

155	RESULT 13 US-10-027-632-111991/C US-10-027-632-111991/C Sequence 11991, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION NUMBER: US 60/218,006 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR APPLICATION NUMBER: US 60/195,218 PRIOR APPLICATION NUMBER: US 60/195,363 PRIOR PILING DATE: 2000-03-29 PRIOR PILING DATE: 1999-11-23 PRIOR PILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28	SOFTWARE: FastSEQ for Windows Version 4.0     SEQ ID NO 111991	10-053-410-4 (1-206) x US-10-027-632-111991 (1-2988)  44 SerProLeuAspalaCyBArgGlnValLeuAspArgGlnLe [
Qy         181 yrAlaalaGlyLoperoArg1leGlyArgValArgLeuThrLysAlaArgGluT 181           Db         120 CCGCGGGTCGCCGCGCGCCCCCCGACGGGCCGGCCGC 82           Qy         181 yrAlaalaGlyLeuProMetMetCysArgLeuSerGluProGlnGluCysSerIle 199           Db         81 GAGCGCGCGCGCCCCGGTCCCGGTGAGTGTTTGTA 44           RESULT 12         11           US-10-027-632-140092/c         3 Sequence 140092/c           Sequence 140092, Application US/10027632	GENERAL INFORMATION: APPLICANTY Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Delymorphisms in the Human Genome FILE REFERENCE: 108827.129 FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR PILING DATE: 2000-07-12 PRIOR FILING DATE: 2000-07-20 PRIOR PILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR PLING DATE: 1000-02-24 PRIOR PLING DATE: 1000-02-24 PRIOR PLING DATE: 1000-02-24 PRIOR PLING DATE: 1099-10-23 PRIOR PLING DATE: 1999-09-28 PRIOR PLING DATE: 1999-09-28 PRIOR PLING DATE: 1999-09-28 PRIOR PLING DATE: 1999-09-28 PRIOR PLING DATE: 1999-09-38 PRIOR PLING DATE: 1990-09-38	res: arity: milari -4 (1- ThrGl	65 GlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGln-GlnLeuGl 84 [

0	Alignment Scores: 0.0485 Length: 3031  Pred. No.: 118.50 Matches: 57  Scoret Similarity: 33.85\$ Conservative: 8  Best Local Similarity: 29.69\$ Mismatches: 45  Query Match: 10.32\$ Indels: 12  DB:
114	Oy 44 SerProLeuAspalaCysArgGlnValLeuAspArgGlnLeuThrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG

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-----GATACGGCC 2845
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2724 CAAGCGCCCTACCGGGAGCTGCTGCTGAAGCACATGCAGCATGAGAACGTAGGTGG 2665
                                                                  ------cascreccagresagesicas 2866
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                                                                                                                                                                                                                                                                                                                                                                      134 TyrTyrTyrProCysSerArgProGlyGluGlyTyrGly------TyrGlyGln 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 -GlyGlyGlnArgGlnMetTyrProProCysArgProGlyThrThrGlyGlyGlyProAr 169
                                                                                                                                                                                                                                                                                                     169 gilediyargValargieuThrLysAlaArgGluTyrAlaAlaGlyLeuProMetMetCy 189
                                  44 SerProLeuAspAlaCysArgGlnValLeuAspArgGlnLeuThrGlyGlyGlyGlyGly 63
                                                                                                 64 GlyGlyValGlyProPheArgTrpGlyThrGlyLeuArgMetArgCysCysGlnGlnLeu 83
                                                                                                                                                                    GlnAspValSerArgGluCys-----ArgCysAla-----AlaIleArgSerMet 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2586 crcgggacagrcr-----ccrccrgcrccccrgac-----
                                                                                                                                                                                                                                   99 ValArg------GlyTyrGluGluAlaMetProProLeu
US-10-053-410-4 (1-206) x US-10-027-632-115601 (1-3031)
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                                                2904 AGTCCCTCTCAGCC-----
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